User Manual for IMBA Expert™ OCAS/ORAU-Edition

(Version 4.0)

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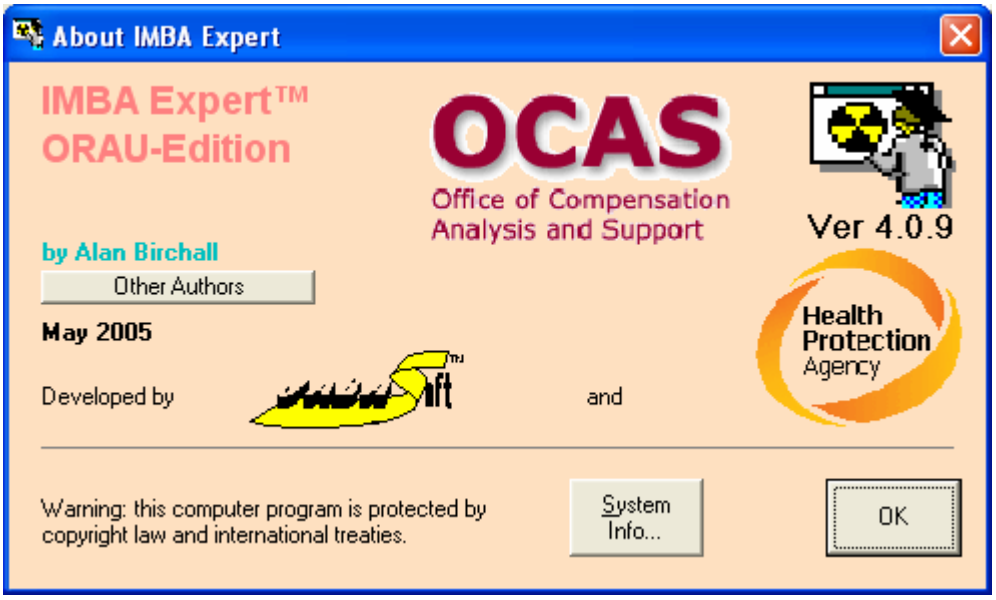
PREFACE

What IMBA Expert™ Does

IMBA Expert™ is a Windows® software application, in several customized editions, written in Visual BASIC® 6.0. The software package provides user-friendly interfaces with the UK National Radiological Protection Board's (NRPB's) proprietary suite of **I**ntegrated **M**odules for **B**ioassay **A**nalysis (**IMBA**). These software applications automatically apply the NRPB's extensively quality-assured **IMBA** code modules to estimate single or multiple intakes of **various radionuclides**, and to calculate the resulting doses from measurements of activity in the body and/or excreta. The **IMBA** code modules implement all of the International Commission on Radiological Protection's (ICRP's) currently recommended respiratory tract, GI-tract, tissue dosimetry, biokinetic and bioassay models for the selected radionuclides, for the ICRP68 Reference Worker. They also implement a generic wound model (for transdermal intake).

What OCAS/ORAU-Edition (Version 4) Does



IMBA Expert™ OCAS/ORAU-Edition is designed for use by the CDC/NIOSH Office of Compensation Analysis and Support (OCAS) and authorized contractor health physicists in support of the CDC-NIOSH Dose Reconstruction under the Energy Employees' Occupational Illness Compensation Program Act (EEOICPA). Under **EEOICPA**, NIOSH (or authorized contractor health physicists) will evaluate the internal radiation doses received by workers using individual worker and workplace monitoring information. The IMBA Expert™ OCAS/ORAU-Edition is a computerized instrument designed to perform the complex calculations of estimating a worker's intake of radioactive materials and converting this intake to an annual dose to a designated target organ or tissue. The annual doses are calculated in a form suitable for input to the **I**nteractive **R**adio**E**pidemiological **P**rogram (NIOSH-IREP) for the purpose of evaluating the probability that an employee's cancer was caused by his or her individual radiation dose. The

calculations performed by IMBA Expert™ OCAS/ORAU-Edition utilize the most recent lung and biokinetic models produced by the International Commission on Radiological Protection (ICRP) which are consistent with the internal dose reconstruction approach being adopted by NIOSH.

IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) is a Windows® software application written in Visual BASIC® 6.0. The software provides an intuitive, user-friendly interface with the UK Health Protection Agency – Radiation Protection Division's (HPA-RPD's) proprietary suite of **I**ntegrated **M**odules for **B**ioassay **A**nalysis (**IMBA**). This software application automatically applies the HPA-RPD's extensively quality-assured **IMBA** code modules to estimate intakes of the following radioelements (112 individual radioisotopes) from measurements of activity in the body and/or excreta. The 35 isotopes shown below in **bold** were added for Oak Ridge Associated Universities (ORAU) under purchase order BPA 7-5445 with ACJ & Associates, Inc.

Radioelement	**Symbol**	**Isotopic Mass Number**
Actinium	Ac	227, 228
Americium	Am	241, 243
Antimony	Sb	124, 125
Arsenic	**As**	**74**
Barium	Ba	**133**, 140
Berkelium	**Bk**	**249**
Calcium	**Ca**	**45**
Californium	Cf	**249**, 252
Carbon[1]	C	14
Cerium	Ce	**139**, 141, **143**, 144
Cesium	Cs	134, 137
Chlorine	**Cl**	**36**
Chromium	Cr	51
Cobalt	Co	57, 58, 60
Curium	Cm	242, 243, 244
Europium	Eu	152, 154, 155, 156
Hafnium	Hf	181
Hydrogen (Tritium)[1,2]	H	3
Iodine	I	125, 129, 131, 133, 134, 135

[1] As particulate. gas or vapor.
[2] Biokinetic models are included for both organically bound tritium (OBT) and tritiated water (HTO).

Iridium	**Ir**	**192**
Iron	Fe	55, 59
Lanthanum	La	140
Lead	**Pb**	**210**
Lutetium	**Lu**	**174**
Manganese	Mn	54
Mercury	**Hg**	**203**
Molybdenum	**Mb**	**99**
Neptunium	Np	237, 239
Nickel	Ni	63
Niobium	Nb	94, 95
Phosphorus	P	32, 33
Plutonium	Pu	238, 239, 240, 241, 242
Polonium	Po	**208, 209**, 210
Praesodymium	**Pr**	**143, 147**
Promethium	Pm	147
Protactinium	Pa	231, **233, 234**
Radium[3]	Ra	**223**, 224, 226, 228
Ruthenium	Ru	103, 106
Samarium	**Sm**	**151**
Scandium	**Sc**	**46**
Silver	Ag	110m
Sodium	Na	22, 24
Strontium	Sr	85, 89, 90, **91**
Sulfur[4]	S	35
Tantalum	**Ta**	**182**
Technetium	Tc	99

[3] Assuming same biokinetic model for parent and radioactive progeny. Note that ICRP68 assumes independent kinetics for the progeny.
[4] As inorganic or organic particulate, gas or vapor.

Tellurium[3]	**Te**	**131, 131m**
Terbium	Tb	160
Thallium	**Tl**	**201, 202, 204**
Thorium[5]	Th	228, 230, 232, **234**
Thulium	**Tm**	**170**
Tin	Sn	113
Uranium[6]	U	**232**, 234, 235, 236, 238, **239**
Ytterbium	**Yb**	**169**
Yttrium	Y	**88**, 90, 91
Zinc	Zn	65
Zirconium	Zr	95

The **IMBA** code modules implement all of the International Commission on Radiological Protection's (ICRP's) currently recommended respiratory tract, GI-tract, tissue dosimetry, and biokinetic models for the reference worker (with the exceptions noted above for progeny of radium, thorium and uranium), and also a wound model (for transdermal intake).

Special Features of OCAS/ORAU Edition

IMBA Expert™ OCAS/ORAU-Edition is a modification and extension of the core IMBA Expert™ code (**IMBA.EXE**) that is designed specifically to meet **NIOSH**'s requirements under the Energy Employees' Occupational Illness Compensation Program Act (EEOICPA, 2000). In particular, IMBA Expert™ OCAS/ORAU-Edition is customized to do the following:

1. **Calculate Equivalent Doses Received by a Specified Organ or Tissue in Each Calendar Year**

   This special functionality enables you to specify:

   - a **target organ** (or tissue) of concern for determining dose related to the probability of cancer causation;
   - the "**start**" date for dose calculation - *i.e.*, the beginning of the occupational internal exposure;
   - the "**end**" date for dose calculation - *i.e.*, the time of diagnosis of the cancer.

[5] Assuming same biokinetic model for parent and radioactive progeny. Note that ICRP68 assumes independent kinetics for the progeny.
[6] Including mixtures of uranium isotopes.

Note: How to use this special feature for calculating annual doses to target tissues is described in "**Special EEOICPA Applications | Dose Calculations for NIOSH-IREP**" – Section 8.1 of this **User Manual**. The preceeding sections describe the operations common to of all versions of IMBA Expert™. These include using the software to manage and analyze bioassay data - and calculating from the bioassay data the associated intakes of radionuclides.

2. Interface with the Interactive RadioEpidemiological Program (NIOSH-IREP)

IMBA Expert™ OCAS/ORAU-Edition reads all claimant identifiers and personal information from an external, standard-format "***.ini**" file. The output report file "***.rpt**" produced by IMBA Expert™ OCAS/ORAU-Edition then includes this claimant information, and is formatted to be read automatically by MJW Corporation's "**FeedIREP**" software. The "***.rpt**" file provides the calculated equivalent doses to a specified target organ (by calendar year), the case details and other claimant information required by "**FeedIREP**" for the latter to produce the standard-format "Claimant Input File" required by the **NIOSH-IREP** computer code.

Note: How to use the special interfaces built into IMBA Expert™ OCAS/ORAU-Edition is described in "**Special EEOICPA Applications**" – Section 8 of this **User Manual** (Section 8.2: "**Input '*.ini' File**" and Section 8.3: "**Output to 'FeedIREP'**"). The preceeding sections describe the operations common to of all versions of IMBA Expert™. These include using the software to manage and analyze bioassay data - and calculating from the bioassay data the associated intakes of radionuclides.

3. Components of Dose Depending on Type and Energy of Emitted Radiation

In order to apply the appropriate weighting factors for risk, to each component of dose delivered to the target organ, NIOSH requires that the calculated doses be broken down into different categories, depending on the type and energy of the emitted radiation. The categories are:

Radiation	Source or Energy
Alpha	All energies
Beta	From tritium
Beta	Other
Gamma	< 30 keV
Gamma	30 keV – 250 keV
Gamma	> 250 keV

Note: The special adaptation of NRPB's **IMBA** modules required to calculate equivalent doses by category of emitted gamma energy is described in the **Appendix A: Technical Basis**, Section A.10. - "**'Split' Gamma SEEs for NIOSH-IREP**".

4. OCAS-Edition (Version 3.2) Extensions to Deal with Additional Radionuclides

In addition to the 62 radionuclide implementations developed for IMBA Expert™ USDOE-Edition (Phase II) and IMBA Expert™ CANDU-Edition, the following radionuclide implementations were developed for OCAS-Edition (Version 3.2) distributed in April 2004:

Radionuclide	Comment
^{227}Ac	-
^{228}Ac	-
^{224}Ra	-
^{226}Ra	-
^{228}Ra	-
^{228}Th	Assume parent kinetics for decay products
^{230}Th	Assume parent kinetics for decay products
^{232}Th	Assume parent kinetics for decay products
^{252}Cf	-
^{243}Cm	-
^{244}Cm	-
^{235}U	-
^{238}U	-
^{91}Y	Added under supplementary contract with ORAU
^{99}Tc	Added under supplementary contract with ORAU
Uranium Mixtures[(1)]	Added under supplementary contract with ORAU

[(1)]Including the ability to specify bioassay measurements in the **mass** unit "**mg**".

Important Note: For ALL gamma-emitting parent (and decay chain) radionuclides implemented in IMBA Expert™ OCAS/ORAU-Edition, the Specific Effective Energy (SEE) file has been split into three categories of emitted gamma-energy, as required by NIOSH.

Common Features of IMBA Expert™

In common with IMBA Expert™ USDOE-Edition (Phase II), the IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) software enables you to do the following.

- Assess intakes from **inhalation**, **ingestion**, **injection** or **transdermal wounds**.
- Calculate **bioassay quantities** as a function of time - implemented quantities are:
  - Whole Body
  - Lungs

- Urine
- Feces
- Blood
- Thyroid
- Liver
- User Defined.

- Calculate simultaneously the best estimates of the **amounts of intake** - from up to ten exposure events (superimposed intake regimes).
- Analyze any of the above types of **bioassay measurement** – for a given indicator radionuclide.
- **Repeating** the calculation with the same assumptions and data yields identical results.
- **Save** all assumptions, parameter values and results to a single, nameable data file – which can be read by any version of IMBA Expert™ (OCAS/ORAU-, CANDU- or USDOE-Editions) or by IMBA Professional Plus (international versions), running on any compatible PC computer system.
- Specify the **date** and **time-of-day** of each bioassay measurement.
- Track time as either date + hh:mm or fractional d.
- Specify the **collection period** for **each** urine and fecal sample (in fraction of a day).
- **Import/export** bioassay data between IMBA Expert™ OCAS/ORAU-Edition and a Windows® **spreadsheet**.
- **Exclude unreliable data points** from the fitting process – but not from the data record – and mark these as such in the associated graph of the data.
- Apply the **maximum likelihood** fitting method - to deal with:
  - data recorded as “less than the limit of detection” (**< LOD**);
  - explicit error on **each data point**;
  - **normal** or **lognormal** error distributions;
  - up to **200 data points**;
  - up to **10 intake regimes simultaneously**.
- Calculate the **committed equivalent dose to each organ** or **tissue** - and the **effective dose** - from both an **indicator radionuclide** and any **associated radionuclides**.
- Toggle between ICRP26, **10 CFR 835**, or ICRP60/68 **tissue weighting factors** and **remainder tissue rules**.

- Create a comprehensive **report file** containing administrative details, all case parameter assumptions, and the calculated results.

- Define all **absorption parameter values** and **aerosol characteristics** - or select the absorption parameters from a built-in database of ICRP-recommended values.

- Define **bioassay retention functions** - or select these from a **database** of ICRP-recommended values.

- Enter **user specified particle transport rates** (in the respiratory tract) - and perform calculations for both **Reference Worker** (light activity) and **heavy activity**.

- Apply **built-in ICRP biokinetic models** for each radioelement - or specify **user-defined models**.

- Display **bioassay data** (with their **error bars** and **fitted bioassay function**) graphically **on-screen** - in multiple windows.

- Interchangeably display **tables** of **bioassay data** and **predicted bioassay quantities** with **graphs** of the same quantities.

- Use **built-in**, highly flexible, **graphical** and **spreadsheet** tools to facilitate **setting up your graphs** and **data entry**.

- Copy **data to-and-from spreadsheets** and other Windows® applications.

- Copy **data to-and-from an ASCII file**.

- Deal with **chelated intakes** – by marking and excluding "treatment-enhanced" excretion data from the intake assessment.

- Apply the built-in **ICRP Publication 38 radiation database** - and view complete decay chains and nuclear data on-screen.

- Toggle between **pCi** and **Bq** activity units.

- Calculate **bioassay quantities over specified time intervals** - for design of future monitoring programs.

- **Save and reload** all assumed parameter values and calculated results for a particular case study in a **comprehensive parameter file**.

IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) also includes the following advanced dosimetry and bioassay analysis options:

- Choose to **include or exclude nuclear recoil energy** from the SEEs of a-emitting radionuclides. ICRP did not choose to include nuclear recoil energy when calculating the dose coefficients published for occupational radiological protection.

- Choose to **optimize complex dosimetry calculations** involving multiple intakes and radioactive progeny for accuracy or speed.

- Choose the "**Bayesian Approach**" – to take account of "**prior**" beliefs about exposure conditions, and/or the measurement history of other individuals (*i.e.*, an exposure cohort).

- Calculate the **uncertainty** in the estimate of intake (for a single intake) - using the least squares fitting method, where every data point is associated with an explicit error value.

- Estimate **intakes of ^{239}Pu** (containing a known **fraction of ^{241}Pu** activity at the time of intake) from measurements of **^{241}Am activity in the lungs**.

- Treat comprehensively the bioassay and internal dosimetry of **tritium**.

The following documentation is included:

  - **User's Manual** (software interactive HTML and hard-copy report).
  - Appendix A – **Technical Basis** (software interactive HTML and hard-copy report).
  - Appendix B – **Bioassay Quality Assurance** (hard-copy report).
  - Appendix C – **Dose Quality Assurance** (hard-copy report).
  - Appendix D - **Example Cases** (hard-copy report).

Authors and Acknowledgements

Dr. Alan Birchall (NRPB/HPA-RPD, UK) designed the user interface, wrote the IMBA Expert™ code, and managed the NRPB/HPA-RPD software development team.

Dr. Tony James (ACJ & Associates, Inc.) was responsible for technical and contractual liaison with the Centers for Disease Control (CDC), National Institute for Occupational Safety and Health (NIOSH), Office of Compensation Analysis and Support (OCAS) sponsors of the IMBA Expert™ OCAS-Edition Phases I and II projects, and with the Oak Ridge Associated Universities (ORAU) Team Dose Reconstruction Project for software enhancements ## 1 through 4. He was also responsible for overall design and development of these projects, software testing, quality assurance, and documentation.

Dr. James Marsh (NRPB/HPA-RPD, UK) managed the development of new and/or improved organ retention and excretion functions, software testing and quality assurance, and helped with code development.

Ms. Denise Dorrian, Ms. Katie Davis, Tony Smith and David King (NRPB/HPA-RPD, UK) carried out the development of organ retention and excretion functions and the software "benchmark" testing.

Dr. Alan Phipps and Mrs. Tracy Smith (NRPB/HPA-RPD, UK) ran the HPA-RPD's **PLEIADES** code to benchmark IMBA Expert™'s calculations of doses and excretion rates.

Dr. Naomi Jarvis (US Consultant) developed the extensions of HPA-RPD's **IMBA Suite** needed for IMBA Expert™ to perform its specialized calculations.

Tony Riddell (Westlakes Research Institute, UK) and Mark Peace (British Nuclear Fuels Limited, UK) authored the **IMBA** code module **"BNFL.FIT"** that implements the maximum likelihood fitting method.

Dr. Matthew Puncher (NRPB/HPA-RPD, UK) was responsible for developing tools and Active-X controls used by IMBA Expert™, and also for validating parts of the code.

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USER MANUAL

1. How IMBA Expert™ Works

All calculations in IMBA Expert™ OCAS/ORAU-Edition are performed from just **three main screens**:

- the ***Main Screen*** (opening screen);
- the ***Bioassay Calculations*** screen;
- the ***Dose Calculations*** screen.

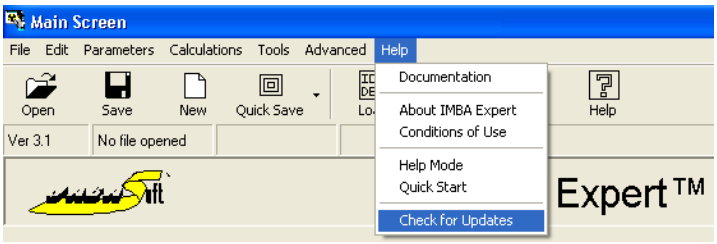
Throughout the operation of IMBA Expert™ OCAS/ORAU-Edition, the currently selected screen remains on the **desk-top** - unless you choose to minimize it. You can move easily (backwards and forwards) between the ***Main Screen*** and either of the "***Calculations***" screens, without losing any data settings. The basic design philosophy is to give you ready access - from the minimum number of screens - to all of your information about intake scenarios, model assumptions, bioassay data, predicted bioassay quantities, and calculated doses. As you proceed through the various functions of the IMBA Expert™ OCAS/ORAU-Edition, the **focus** switches temporarily to smaller overlaid windows. These display your selected parameter values and/or your available selection options. Once you have made your selections, these secondary windows are closed automatically, so that your working screen does not become cluttered. However, the choices that you have made are updated automatically in the ***Status Bar*** or on a "**Tab**" labeled file-card, as appropriate. So, it is very easy for you to locate and re-open any secondary parameter window - to check or change any of your parameter settings.

1.1. Getting User Support

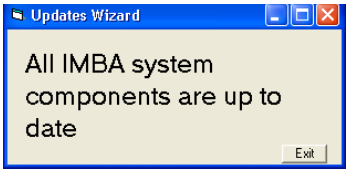
If you experience a problem in using IMBA Expert™ OCAS/ORAU-Edition, or have a suggestion for improving its functionality, please contact ACJ & Associates, Inc.'s *Technical Support Desk* at www.imbaexpertsupport.com. Use the *link* on *that* page to complete the ***OCAS/ORAU User Feedback Form***. The *link* looks like:

OCAS Office of Compensation Analysis and Support	**Show User Feedback Form** - **All Users of IMBA Expert™ *OCAS/ORAU-Edition*** - Please report ANY problem that you encounter in running the software by completing the **User Feedback Form**. Click the "**OCAS**" icon (left) to load the form. Your report will be e-mailed to our Support Desk. **NB:** Don't forget to attach your "***.ix**" file.

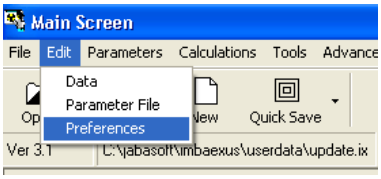
1.2. Software Updates



IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) has a new '**Check for Updates**' feature - accessible in the '**Help**' menu. *Clicking* '**Check for Updates**' will check the web for available updates - and open the '**Updates Wizard**'. This displays the current status of your software installation. If updates are available the 'Updates Wizard' will list these for you - and allow you to *select* those you want to *download*. Installation of the downloaded updates is then done automatically.



Alternatively, you can select to have IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) check the web **automatically** each time you start the program - from the **Edit | Preferences** menu.



2. "What's This?" - Visual Tour

This **tour** will **guide** you through the layout and operation of the IMBA Expert™ OCAS/ORAU-Edition's three working screens, and the tools provided for data entry, export, and visualization, as follows:

1.	**Main Screen** (Opening Screen).
2.	**Bioassay Calculations** Screen; - **Table Tool** (for data entry, editing, export) - **Graph Tool** (for data visualization).
3.	**Dose Calculations** Screen.

2.1. Main Screen (Opening Screen)

The ***Main Screen*** (opening screen) appears when you *click* the **IMBA Expert (ORAU)** icon - which runs **IMBA.exe**. This screen is shown in Figure 2.1.

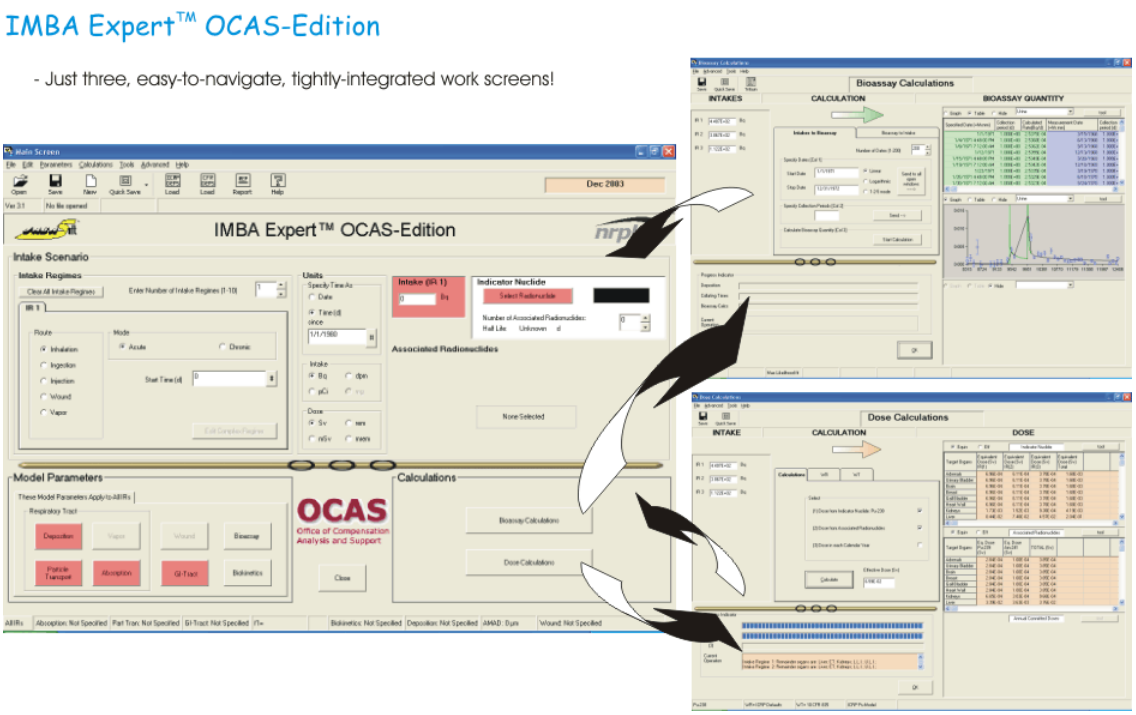


Figure 2.1. **Main Screen** with links to the **Bioassay Calculations** and **Dose Calculations** screens.

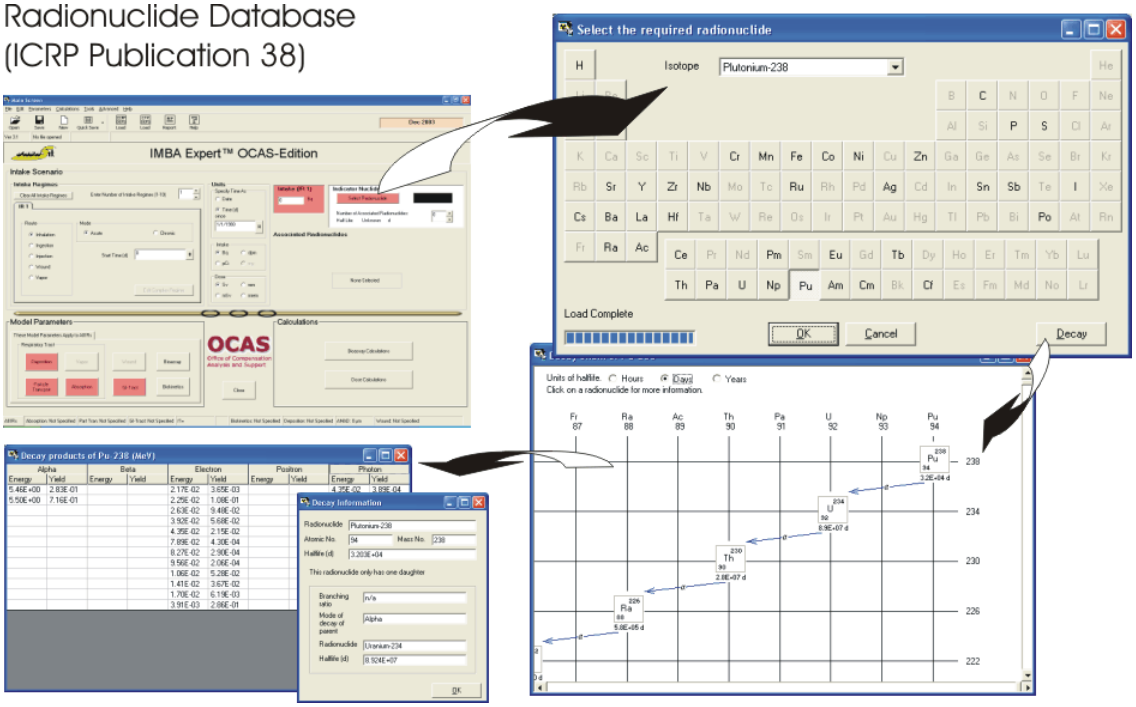


Figure 2.2. Selecting an **Indicator Nuclide.**

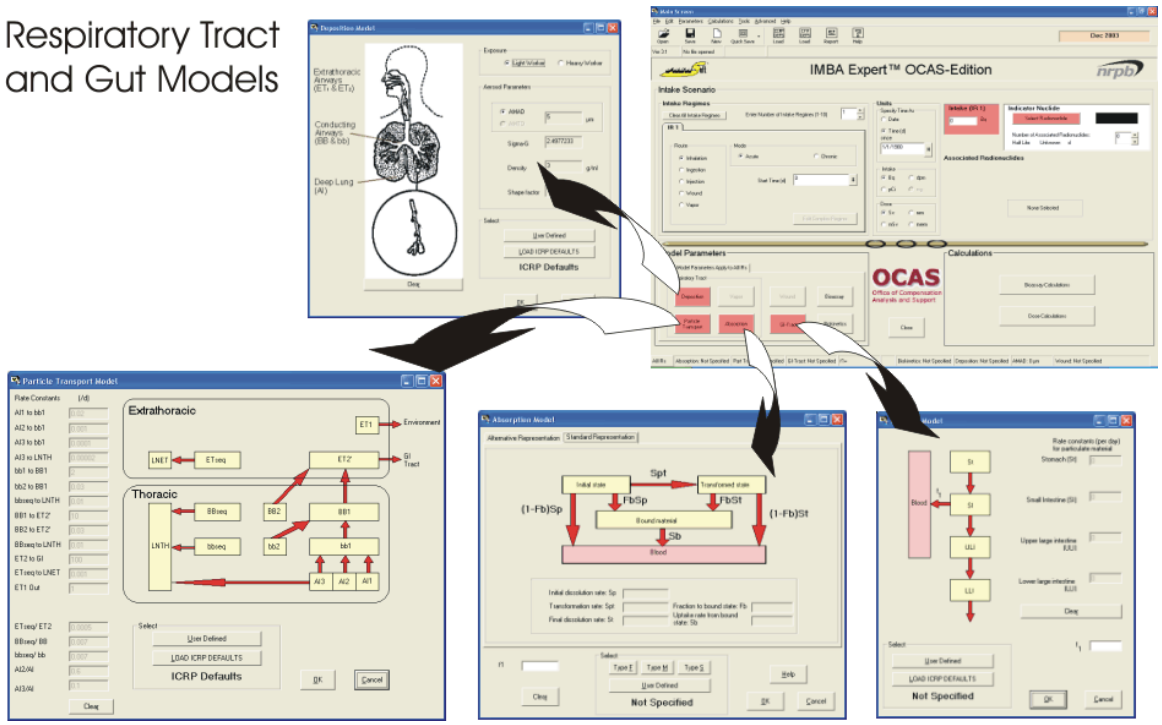


Figure 2.3. Defining the **Respiratory Tract** and **GI Tract** (gut) models.

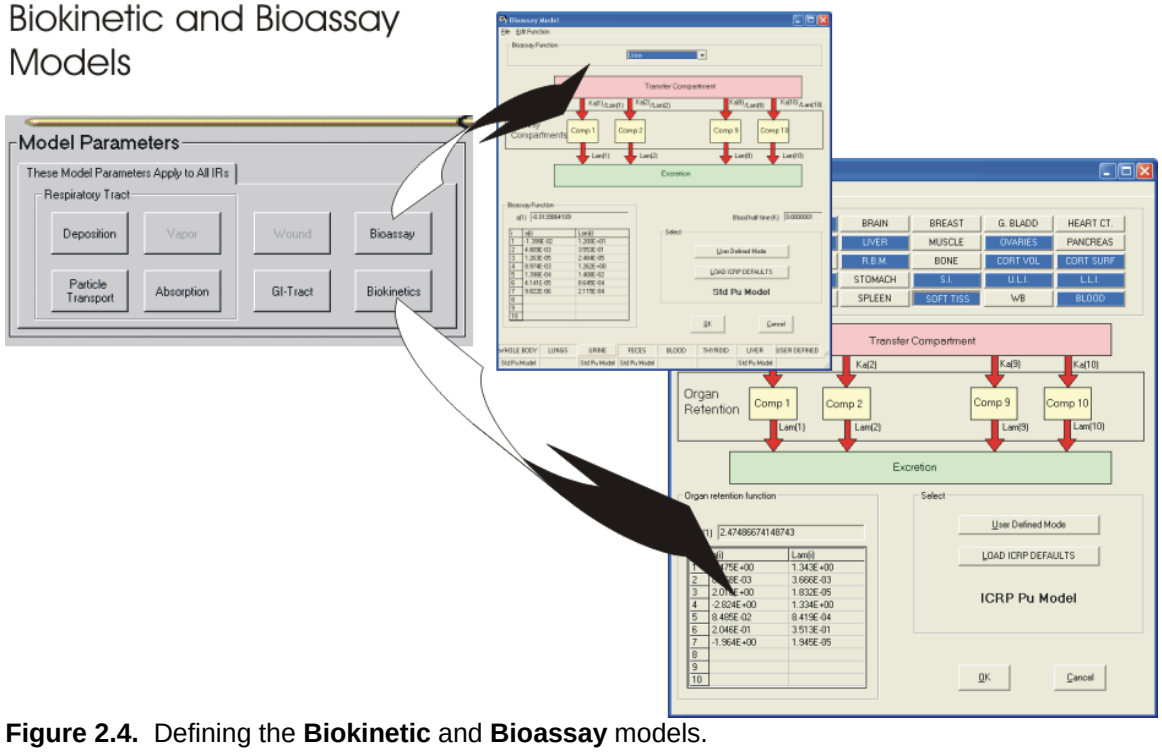


Figure 2.4. Defining the **Biokinetic** and **Bioassay** models.

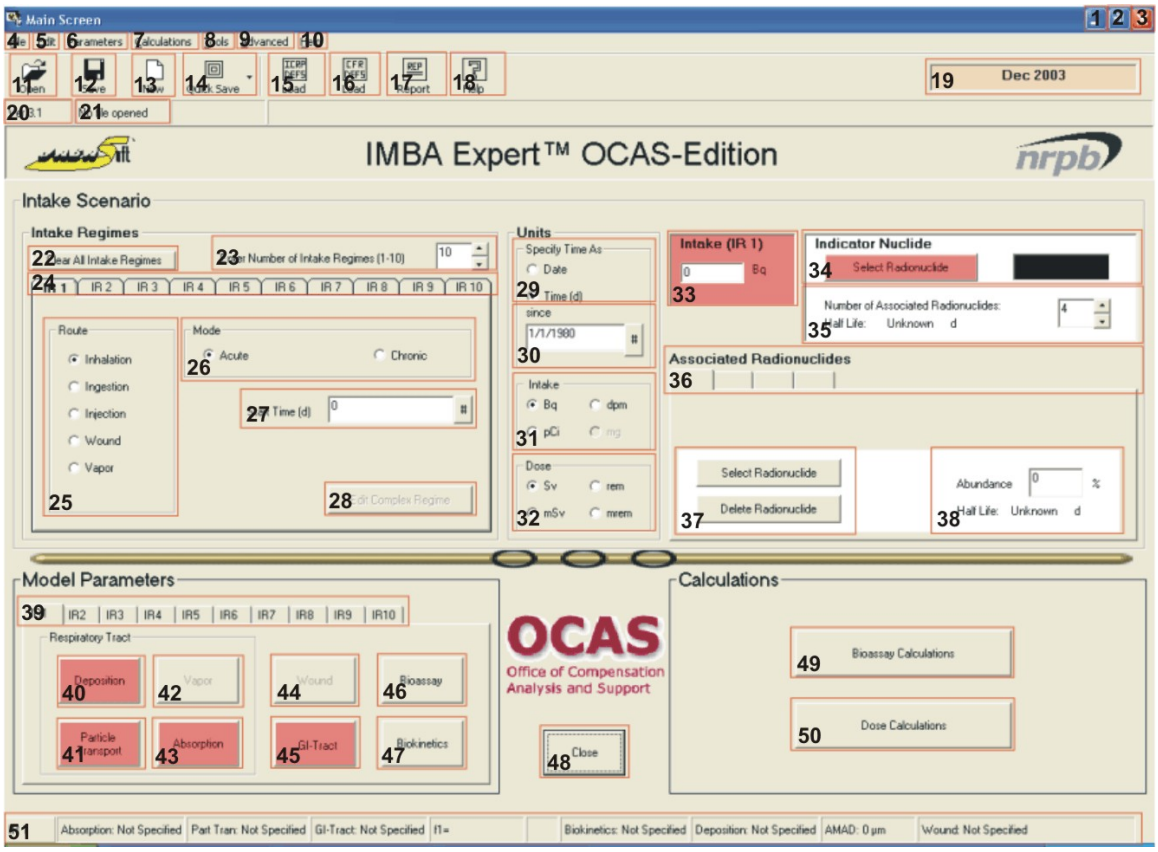


Figure 2.5. What's in the **Main Screen**?

2.1.1. Key to What's in the Main Screen

1. **Minimize:** This minimizes the program display to a button on your task bar - the program will continue to run.
2. **Reduce to Window:** This reduces the size of the **Main Screen** to a window.
3. **Exit Without Saving:** This exits the program - without saving any recent updates of parameter values or calculated results to the **Parameter File** - use with caution!
4. **Main File Menu:** Select from (1) **New** - open a blank Parameter File (for a new case study) – this clears all previous parameter values and calculated results; (2) **Open** - browse the **UserData** folder (or your own data folder) to open a named Parameter File; (3) **Save** - save the current Parameter File (with the current filename); (4) **Save As** - save the current Parameter File with a New filename; (5) **Quick Save** - save the current set of parameter values to the default file named Parameters.ix; (6) **Quick Load** - reload the Parameters.ix file; (7) **Create a Report** - write all or a sub-set of parameter values and calculated results to a named RPT file; (8) **Exit** - unload from memory and exit IMBA Expert™.
5. **Main Edit Menu:** Select to edit **Data** - by opening the **Bioassay Calculations** screen in the **Intakes to Bioassay** mode; Edit **Parameter File** - by opening the current **Parameter File** in **Microsoft Notepad**; Change **Preferences** – choose to play theme tune at startup.
6. **Main Parameters Menu:** Select to **Open** (1) the **Model Parameters** window - for the **HRTM Particle Transport Model**; (2) the **HTRM Absorption Model**; (3) the **HRTM Deposition Model**; (4) the **ICRP30 GI-Tract Model**; (5) the **Bioassay Model** (for the selected radioelement and bioassay quantity); (6) the **Biokinetic (Systemic) Model** (for the selected radioelement); (7) the **Vapor Model**; (8) the **Wound Model**.

7. **Calculations Menu:** Select to **Open** the **Bioassay Calculations** screen; or **Open** the **Dose Calculations** screen.
8. **Main Tools Menu:** This enables you to **Open** the standard **Windows Calculator**; **Open** an untitled file in **Microsoft Notepad**; **Load ICRP Defaults** - *i.e.,* all ICRP-recommended parameter values; **Load 10CFR835 Defaults** - *i.e.,* all parameter values recommended in the current U.S. Department of Energy (DOE) Regulations.
9. **Main Advanced Menu:** Click to **Toggle** the default option to **Apply Model Parameters to All Intake Regimes (IRs) - off/on**; **Enable DOS preview** - this function is primarily for use in debugging program errors; Select **Advanced Dosimetry Options** – choose to exclude nuclear recoil energy from SEEs for alpha emissions.
10. **Main Help Menu:** Click to **View HTML Documentation**; **View** the **About IMBA Expert™** splash screen; **View** the **Conditions of Use**; Select the **Help Mode** - *i.e.,* Toggle on/off 'Mouse-Over' help; **View** the **Quick Start Guide**.
11. **Open Tool Button:** Browse to open a named **Parameter File** - from the **UserData** folder or your own folder location.
12. **Save Tool Button:** Save the current **Parameter File** - if the file has not yet been named, the **Save As** dialog box will open.
13. **New Tool Button:** Clear all parameter values and case data and open a blank **Parameter File** - use with caution!
14. **Quick Save/Load Tool Button:** Save the current **Parameter File** to the default **Parameters.ix** name and location - or Load the **Parameter.ix** file.
15. **Load ICRP DEFS Tool Button:** Quick-load **ALL ICRP-recommended models** - you will be prompted to define discretionary values - *e.g.,* the gut uptake fraction, f_1.
16. **Load CFR DEFS Tool Button:** Quick-load **ALL ICRP-recommended models** together with **10CFR835** prescribed tissue weighting factors and remainder tissue rules - you will be prompted to define discretionary values - *e.g.,* the gut uptake fraction, f_1.
17. **Report Tool Button:** Open the **Report** window to compose and **Save** a named case report.
18. **Help Tool Button:** View a scrollable summary of available **Help options**.
19. **Version Date:** This is the date of the last major software update – as supplied to the User, or as downloaded later *via* an updated "IMBA.ZIP" file.
20. **Software Edition:** This is the **Primary Version Number** - see **Help | About IMBA Expert** for the full **Version Control Number**.
21. **Parameter File Name/Location Box:** This box displays the **Name** and **Location** of the current **Parameter File**.
22. **Clear All Intake Regimes:** This clears all of the displayed **Intake Regime** parameters, and restores the default initial setting of an undefined single intake (IR1) - use with caution!
23. **Number of Intake Regimes:** Define up to **10 Intake Regimes** that you want to analyze simultaneously - the **default** is **IR1**.
24. **Intake Regime Tabs:** IMBA Expert™ automatically sets up a **Tab** for each individual **Intake Regime**.
25. **Route of Intake:** Select this independently for each **Intake Regime** - choose from **Inhalation**, **Ingestion, Injection, Wound** or **Vapor**.
26. **Mode of Intake:** Select whether the **Intake** is **Acute** or **Chronic**.
27. **Start and End Time:** Enter the **Start Time** (or **Date** with hh:mm, as appropriate) for each **Intake Regime**. If the IR mode has been defined as **Chronic**, a second dialog box is automatically displayed for you to enter the **End Time** - or **End Date**.
28. **Edit Complex Regime:** This feature is not implemented in Version 3.2.
29. **Specify Time Units:** Select **Date** (which can include hh:mm); or **Select Time** (d) as the unit in which time is displayed - the **Bioassay Calculations** screen automatically displays time in your selected unit.
30. **Reference Date:** When **Time** (d) is selected as the unit of time, all times are tracked (*e.g.*, for graph plotting) with respect to this **Reference (Since) Date + hh:mm** - Date + 00:00 is assumed if not otherwise specified.

31. **Activity Units:** Select from **Bq**; **dpm** (disintegrations per minute); **pCi** - the bioassay quantity is automatically expressed in the corresponding unit and values of dose are automatically calculated accordingly. The '**mg**' unit (greyed out) must be selected in the **Bioassay Calculations** screen.
32. **Dose Units:** Select from **Sv**; **mSv**; **rem**; **mrem** - the selected unit is used to display both equivalent and effective doses.
33. **Intake Amount (by Regime):** This box displays the **Amount** of **Intake** for the selected **Intake Regime** (IR) - this can be a hypothetical (entered) amount, or the amount calculated from bioassay data.
34. **Indicator Nuclide:** Click the **Select Radionuclide** button to open the periodic table of elements showing the available radioelements/radionuclides - a single indicator nuclide must be defined for each case study.
35. **Number of Associated Radionuclides:** Select the number (if any) of **Associated Radionuclides**. These radionuclides are assumed to be associated with every intake.
36. **Associated Radionuclide Tabs:** These display automatically the names (if any) of the selected **Associated Radionuclides**.
37. **Select Associated Radionuclides:** Select each **Associated Radionuclide** (from the periodic table of elements) or **Delete** any previously selected radionuclide.
38. **Define Abundance of Associated Radionuclide:** Enter the **Abundance** (in %) of an **Associated Radionuclide** relative to the **Activity** of the **Indicator Nuclide**.
39. **Independent IR Model Parameters:** IR# **Tabs** appear in the **Model Parameters** panel when you un-check the **Apply Model Parameters to All IRs** option in the **Advanced Menu** - these IR# Tabs enable you to specify independent model parameters for each **Intake Regime**.
40. **Deposition Model Button:** Click to open the **HRTM Deposition Model** window - to define the aerosol characteristics and select **Reference Worker** (default) or **Heavy Worker** - for an **Intake** by **Inhalation**.
41. **Particle Transport Model Button:** Click to open the **HRTM Particle Transport Model** window - to load ICRP-recommended values, or define your own value of any rate constant - for an **Intake** by **Inhalation**.
42. **Vapor Model Button:** Click to open the **HRTM Vapor Model** - for Intake of a **Vapor**.
43. **Absorption Model Button:** Click to open the **HRTM Absorption Model** window - to select an ICRP-default absorption model, or define your own absorption rates for a specific material - for an **Intake** by **Inhalation**.
44. **Wound Model Button:** Click to open the **Wound Model** window - to define the retention characteristics of the material at the wound site - button is activated automatically when **Wound** is selected as the **Route of Intake**.
45. **GI-Tract Model Button:** Click to open the **ICRP30 GI-Tract Model** window to load the ICRP-default model and select (or confirm) the value of the gut uptake fraction, f_1 - or define your own values of rate constants - for an **Intake** by **Inhalation** or **Ingestion**.
46. **Bioassay Model Button:** Click to open the **Bioassay Model** window to select and load the ICRP-recommended **Bioassay Function** (for the bioassay quantity of interest) - or define your own Bioassay Function - with great caution! Note in particular that a consistent biokinetic model must also be defined.
47. **Biokinetic Model Button:** Click to open the **Biokinetics Model** window to select and load the ICRP-recommended **Biokinetic Model** (for all source organs/tissues for the selected radionuclide) - or define your own Biokinetic Model - with great caution!
48. **Close Button:** This **Saves** all current parameter values and calculated results to the current **Parameter File**, then **Unloads** and **Exits** IMBA Expert™.
49. **Open Bioassay Calculations Screen:** This opens the **Bioassay Calculations** screen with full-screen display.
50. **Open Dose Calculations Screen:** This opens the **Dose Calculations** screen with full-screen display.
51. **Main Status Bar:** This indicates the loaded values of **Model Parameters** (*i.e.,* the selected **ICRP-default values**, and any **User Defined** values) - for the indicated **IR**.

2.2. Bioassay Calculations Screen

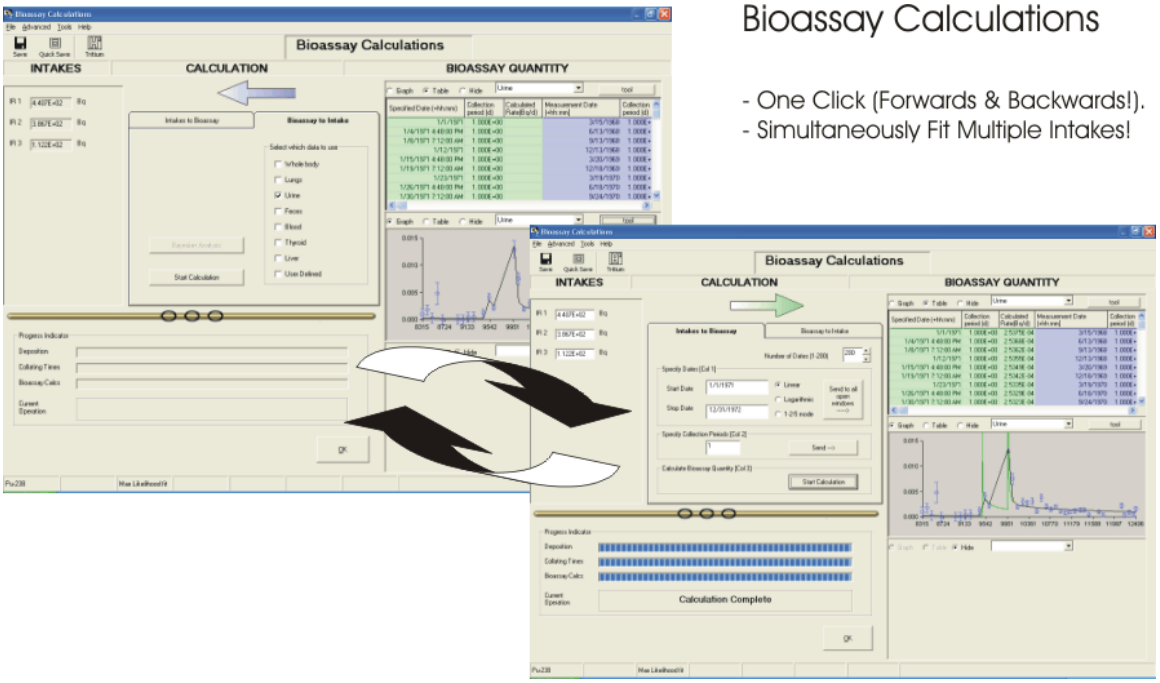


Figure 2.6. The **Bioassay Calculations** screen operates in **two modes** – forwards (from **Intakes** to **Bioassay Quantity**) and backwards (from **Bioassay Quantity** to **Intakes**).

2.2.1. Bioassay Quantity to Intakes Screen Mode

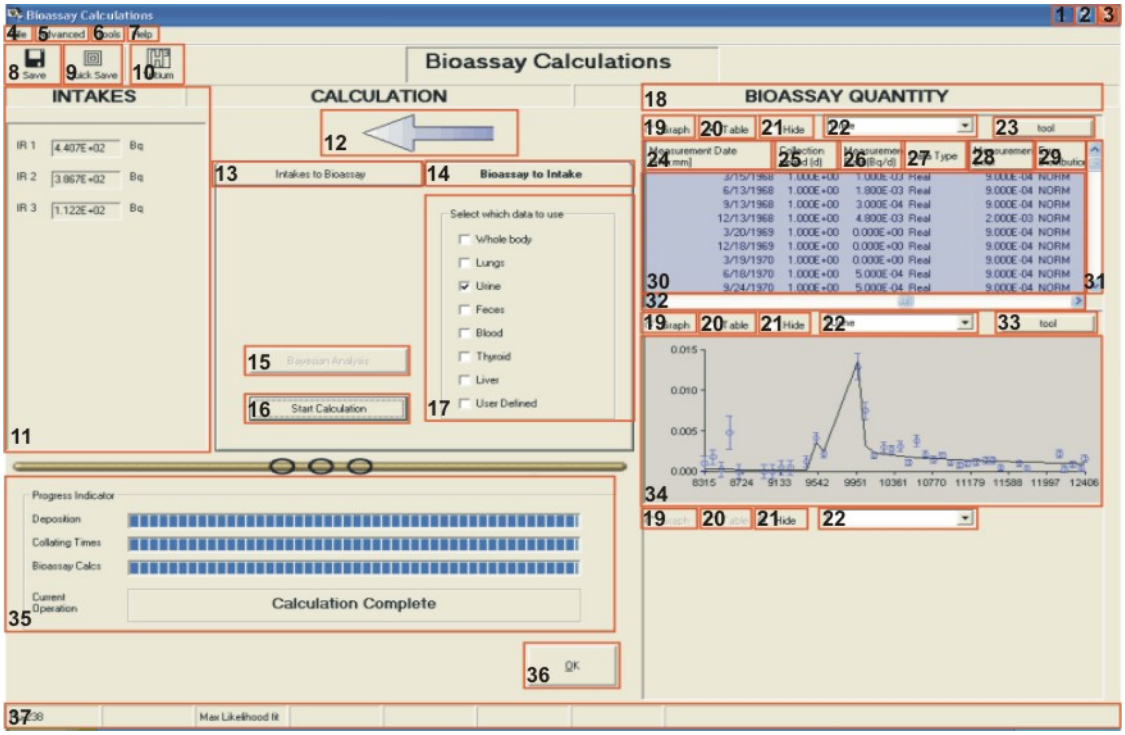


Figure 2.7. What's in **Bioassay Calculations**? – **Bioassay Quantity to Intakes** mode.

Key to Bioassay Quantity (BQ) to Intakes Mode

1. **Minimize Bioassay Screen:** Not used.
2. **Reduce Bioassay Screen:** This reduces the size of the **Bioassay Screen** to a window - visible on top of the **Main Screen**.
3. **Exit Bioassay Screen:** This exits the **Bioassay Screen** and returns you to the **Main Screen** - without saving changes made to the bioassay data since last saving the **Parameter File**. Use with caution!
4. **File Menu (Bioassay):** Drop-down options to (1) **Save** - save the current **Parameter File** (with the current filename); (2) **Save As** - save the current **Parameter File** with a **New** filename; (3) **Print** - print a **screen dump** of the currently displayed **Bioassay Calculations** screen.
5. **Advanced Menu (Bioassay):** Select (1) **Fitting Options** - **Least Squares** method, **Maximum Likelihood** method (default), or **Bayesian Analysis**; and (2) **Bioassay Option** - special feature to calculate **in-growth of ^{241}Am activity in the lungs** from an intake of plutonium isotopes (containing a known fraction of ^{241}Pu activity).
6. **Tools Menu (Bioassay):** Drop-down options to (1) **Open Table Tool** (for BQ Window 1, 2 or 3); (2) **Open Graph Tool** (for BQ Window 1, 2 or 3); (3) **Toggle Units** between **Time** and **Date**; (4) **Display Statistics** - not used; (5) **Routine Tritium Monitoring** - use a special spreadsheet-like tool (window) to analyze data from **routine monitoring of tritium-in-urine**.
7. **Help Menu (Bioassay):** Same options as **Help Menu** in **Main Screen** - (1) View **HTML Documentation**; (2) View **About IMBA Expert™**; (3) View **Conditions of Use**; (4) Select **Help Mode**; (5) View **Quick Start Guide**.
8. **Save Icon (Bioassay):** Click this to **Save** all current bioassay values and calculated results in the currently open **Parameter File** (*.ix).
9. **Quick Save (Bioassay):** Save the current **Parameter File** - including all changes to the bioassay data - to the default **Parameters.ix** file name and location.
10. **Tritium Tool:** Use a special spreadsheet-like tool (window) to analyze data from **routine monitoring of tritium-in-urine**.
11. **Intake Panel (B to I):** In the **"Bioassay to Intake"** mode, this **displays** the **calculated values of intakes**.
12. **Calculation Arrow (B to I):** The blue/white arrow indicates that the calculation will go from the measured bioassay data - *i.e.*, the values in the blue columns of the **Bioassay Quantity** table - to the estimated **Intake** amount(s) - to be displayed in the Intake(s) dialog box(es). Click the **Arrow** to reverse the direction of calculation!
13. **Intakes to Bioassay Tab (Selectable):** Click this to change the direction of the calculation to go from defined amounts of **Intake** to predicted **bioassay quantities** - or click the **Arrow** to reverse its direction.
14. **Bioassay to Intakes Tab (Active):** Indicates that the **bioassay data** selected in the panel below the tab will be used to estimate (simultaneously) the values of all defined **Intake(s)**.
15. **Bayesian Analysis Button:** Enables you to analyze bioassay data using **Bayesian inference**, whereby a sampling distribution is first postulated that relates the unknown parameters to the measurements, and a **prior distribution** is postulated for the unknown parameters. The prior distribution expresses subjectively our uncertainty in the values of the unknown parameters, before the measurements are used. To the extent that the information embodied in the prior distribution accurately reflects the uncertainty about the parameters, Bayesian inference produces better estimates of the unknown parameters (*i.e.*, narrower confidence intervals) than classical statistical methods.
16. **Start Calculation (B to I):** Click to start the defined calculation - the results are displayed automatically in Column 9 (grey background) - the far-right column of the **Bioassay Quantity** table.
17. **Select Bioassay Data to Use:** Select one of the ***8*** types of bioassay data to use for the **Intake(s)** calculation - if you select multiple quantities they will be used **simultaneously** to calculate the best single estimate of each intake (for up to 10 separate intakes).

18. **Bioassay Quantity Panel:** This has three windows - in which you can select to display any combination of **tables** and/or **graphs** of **bioassay quantities**.
19. **Show Graph:** Select this to display a **graph** in this **Bioassay Quantity** window.
20. **Show Table:** Select this to display a **table** in this **Bioassay Quantity** window.
21. **Hide Display:** This option is checked automatically until either **graph** or **table** is selected. Click the "hide" option to remove the display.
22. **Select Bioassay Quantity for Display:** Use the arrow to open a drop-down list of all **Bioassay Quantities** - and select the one you want to display in this **Bioassay Quantity** window.
23. **Open Table Tool:** Click this button to open an expanded table of data (**Table Tool**) for the selected **Bioassay Quantity** - the Table Tool has built-in facilities to **enter**, **import**, **edit** and/or **export** data.
24. **Measurement Date Column:** This column displays the **date** (+ time-of-day in hh:mm) for each **measured** value of the **Bioassay Quantity**, *i.e.,* the time-point plotted on the x-axis of the graph - use the **Tool | Change Units to Time** toggle in the **Tool Menu** to change all **Date** values to **Time** (in fractional-d) **Since the Reference Date**.
25. **Collection Period Column:** This column displays the **collection period** for each measured **urine** or **fecal** excretion sample - this can be different for every sample. Values in this column are ignored when the **Bioassay Quantity** is a **measured body activity** (*e.g.,* whole body or lungs).
26. **Measured Rate Column:** This displays the measured **rate** of urinary or fecal excretion (in Activity Unit/d). When the **Bioassay Quantity** is a measured **body activity** (*e.g.,* whole body or lungs), the column heading changes automatically to **Measurement Value** (in Activity Unit).
27. **Data Type Column:** This displays the **type** of each data point - either (1) **< LOD** (less than Limit of Detection); (2) **Real** (reliable measured value); or (3) **Excluded** (unreliable measured value that will be ignored in the fitting procedure).
28. **Measurement Error Column:** This displays the value of the **measurement error** for each data point - plotted as a "**+/-**" bar in the graph.
29. **Error Distribution Column:** This displays the **type of error distribution** for each data point (1) **Normal**; (2) **Lognormal** - you can designate the error distribution as Normal for some data points and Lognormal for others, as appropriate.
30. **Table of Measured BQ Data (B to I):** Five columns (with blue background - Columns 4-8 in the table) display the **measured Bioassay Quantity** values (up to 200 rows, 1 row per data point). Column 9 (grey background) displays the **fitted** value of the **Bioassay Quantity** for each data point.
31. **Scroll Bar:** Use this to view **hidden rows**, *i.e.,* additional data rows below those displayed.
32. **Column Scroll Bar:** Use this to view **hidden data columns**, *i.e.,* the additional blue columns to the right in this window.
33. **Open Graph Tool:** Click this button to open an expanded graph window (**Graph Tool**) for the selected **Bioassay Quantity**. The Graph Tool has built-in facilities to set up your graph - to define the axis-scales and select which measured data and fitted values to plot.
34. **Graph of BQ Data:** Displayed **graph** of the selected **Bioassay Quantity**. The plotted values are selected in the **Graph Tool** - data points, fitted value for each data point (joined by blue lines), and/or the predicted bioassay quantity shown by the green curve.
35. **Bioassay Calculation Progress Indicator:** Indicates the calculation in progress, the proportion of each sequential task completed, and completion of the whole calculation. When the calculation is complete, the results are automatically displayed.
36. **OK Button:** Click to **save all current bioassay values** and **calculated results** in the currently open **Parameter File (*.ix)** - and return to the **Main Screen**.
37. **Bioassay Calculation Status Bar:** This shows (1) the **Indicator Nuclide**, (2) the set of **Radionuclide Bioassay Models** used, and (3) the **Fitting Method** used.

2.2.2. Intakes to Bioassay Quantity Screen Mode

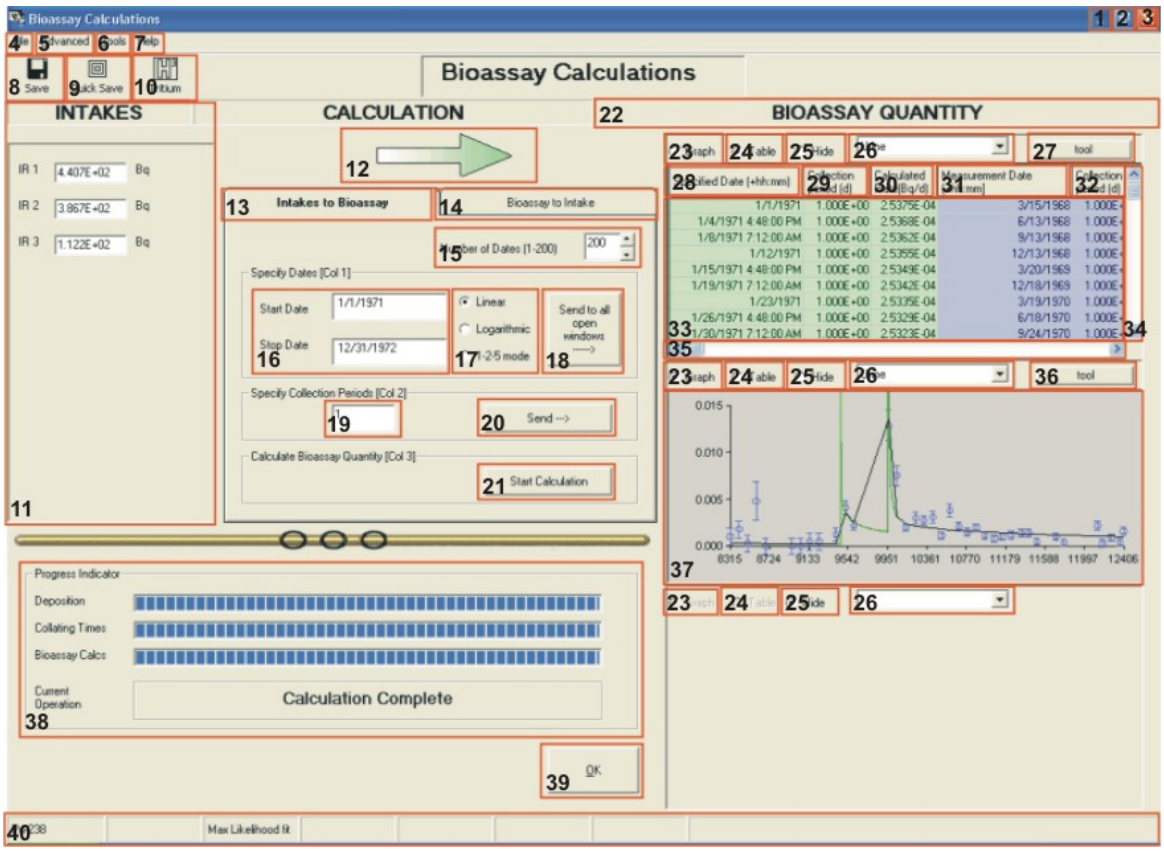


Figure 2.8. What's in **Bioassay Calculations**? – **Intakes to Bioassay Quantity** mode.

Key to Intakes to Bioassay Quantity (BQ) Mode

1. **Minimize Bioassay Screen:** Not used.
2. **Reduce Bioassay Screen:** This reduces the size of the **Bioassay Screen** to a window - visible on top of the **Main Screen**.
3. **Exit Bioassay Screen:** This exits the **Bioassay Screen** and returns you to the **Main Screen** - without saving changes made to the bioassay data since last saving the **Parameter File**. Use with caution!
4. **File Menu (Bioassay):** Drop-down options to (1) **Save** - save the current **Parameter File** (with the current filename); (2) **Save As** - save the current **Parameter File** with a **New** filename; (3) **Print** - print a **screen dump** of the currently displayed **Bioassay Calculations** screen.
5. **Advanced Menu (Bioassay):** Select (1) **Fitting Options** - **Least Squares** method, **Maximum Likelihood** method (default), or **Bayesian Analysis**; and (2) **Bioassay Option** - special feature to calculate **in-growth of ^{241}Am activity in the lungs** from an intake of plutonium isotopes (containing a known fraction of ^{241}Pu activity).
6. **Tools Menu (Bioassay):** Drop-down options to (1) **Open Table Tool** (for BQ Window 1, 2 or 3); (2) **Open Graph Tool** (for BQ Window 1, 2 or 3); (3) **Toggle Units** between **Time** and **Date**; (4) **Display Statistics** - not used; (5) **Routine Tritium Monitoring** - use a special spreadsheet-like tool (window) to analyze data from **routine monitoring of tritium-in-urine**.
7. **Help Menu (Bioassay):** Same options as **Help Menu** in **Main Screen** - (1) View **HTML Documentation**; (2) View **About IMBA Expert**; (3) View **Conditions of Use**; (4) Select **Help Mode**; (5) View **Quick Start Guide**.

8. **Save Icon (Bioassay):** Click this to **Save** all current bioassay values and calculated results in the currently open **Parameter File** (*.ix).
9. **Quick Save (Bioassay):** Save the current **Parameter File** - including all changes to the bioassay data - to the default **Parameters.ix** file name and location.
10. **Tritium Tool:** Use a special spreadsheet-like tool (window) to analyze data from **routine monitoring of tritium-in-urine**.
11. **Intake Panel (I to B):** This displays the value(s) of **Intake(s)** that will be used to **predict** values of the **bioassay quantity** - the number of Intake(s) was set up in the **Main Screen** - up to 10 intakes can be defined.
12. **Calculation Arrow (I to B):** The white/green arrow indicates that the calculation will go from the defined **Intake(s)** - *i.e.,* the values in the white **Intakes** dialog box(es) - to the predicted **Bioassay Quantities** - to be displayed in green (Column 3) in the **Bioassay Quantity** table. Click the **Arrow** to reverse the direction of calculation!
13. **Intakes to Bioassay Tab (Active):** Indicates that the time values defined in the panel below the tab will be used to **predict** the corresponding values of the **Bioassay Quantity** for the defined **Intake(s)**.
14. **Bioassay to Intakes Tab (Selectable):** Click this to change the direction of the calculation to go from **measured bioassay quantities** to estimate(s) of **Intake(s)**.
15. **Number of Dates (I to B):** Define the **Number of Dates** (time points) at which you want to predict the **bioassay quantity** - up to 200 time points can be used.
16. **Specify Dates (I to B):** Enter here the **Start** and **End** dates (and/or times) for the time-series over which you want the **bioassay quantity** to be predicted.
17. **Type of Time Series (I to B):** Select either "**Linear**" or "**Logarithmic**" or "**1-2-5 mode**" (*e.g.,* 1, 2, 5, 10, 20 from within the specified range of dates/times) for the type of time series.
18. **Send Time Series (I to B):** This sends the specified **series of times/dates** to fill Column 1 (green background) in all open **Bioassay Quantity** tables.
19. **Collection Period (I to B):** For **urine** or **feces** as the **Bioassay Quantity**, this is the sample collection period (*e.g.,* 1 day) for which you want to predict the amount of excreted activity in the sample collected at each specified time or date.
20. **Send Collection Period (I to B):** This sends the entered value of **collection period** to fill Column 2 (green background) in all open **Bioassay Quantity** tables.
21. **Start Calculation (I to B):** Click to **start** the defined calculation - the results are displayed automatically in Column 3 (green background) of the **Bioassay Quantity** table.
22. **Bioassay Quantity Panel:** This has three windows - in which you can select to display any combination of **tables** and/or **graphs** of **Bioassay Quantities**.
23. **Show Graph:** Select this to display a **graph** in this **Bioassay Quantity** window.
24. **Show Table:** Select this to display a **table** in this **Bioassay Quantity** window.
25. **Hide Display:** This option is checked automatically until either **graph** or **table** is selected. Click the “hide” option to remove the display.
26. **Select Bioassay Quantity for Display:** Use the arrow to open a drop-down list of all **Bioassay Quantities** - and select the one you want to display in this **Bioassay Quantity** window.
27. **Open Table Tool:** Click this button to open an expanded **table of data** (**Table Tool**) for the selected **Bioassay Quantity** - the **Table Tool** has built-in facilities to **enter**, **import**, **edit** and/or **export** data.
28. **Specified Date Column:** This column displays the **date** (+ time-of-day in hh:mm) for each **predicted** value of the **Bioassay Quantity**, *i.e.,* the time-point plotted on the x-axis of the graph - use the **Tool | Change Units to Time** toggle in the **Tool Menu** to change all **Date** values to **Time** (in fractional-d) **Since the Reference Date**.
29. **Collection Period (for Predicted BQ):** The hypothetical Collection Period is the same for all predicted **urinary** or **fecal** excretion amounts - usually 1 d. You can load this into all data rows with one click from the **Intakes** to **Bioassay Quantities** panel (**Bioassay Calculations** screen) - or simply [Paste] the required value into the whole **Collection Period** column in the **Table Tool**.

30. **Predicted BQ Value Column:** Clicking the [**Start Calculation**] button will calculate the **Bioassay Quantity** values for all defined time-points - and display the results automatically in Column 3. The column heading changes automatically with the selected **Bioassay Quantity**; either (1) **Calculated Rate** (Activity/d) for **urine** or **feces**, or (2) **Calculated Value** (Activity) for **other bioassay quantities**.
31. **Measurement Date Column:** This column displays the **date** (+ time-of-day in hh:mm) for each **measured** value of the **Bioassay Quantity**, *i.e.,* the time-point plotted on the x-axis of the graph - use the **Tool | Change Units to Time** toggle in the **Tool Menu** to change all **Date** values to **Time** (in fractional-d) **Since the Reference Date**.
32. **Collection Period Column:** This column displays the collection period for each measured urine or fecal excretion sample.
33. **Table of Data:** Columns 1-3 (with **green** background) display the **predicted** bioassay quantity values - up to 200 rows, 1 row per data point. Columns with **blue** background display the **measured** bioassay quantity values (up to 200 rows, 1 row per data point).
34. **Scroll Bar:** Use this to view **hidden rows**, *i.e.,* additional data rows below those displayed.
35. **Column Scroll Bar:** Use this to view **hidden data columns**, *i.e.,* the additional blue columns to the right in this window.
36. **Open Graph Tool:** Click this button to open an expanded **graph** window (**Graph Tool**) for the selected **Bioassay Quantity**. The Graph Tool has built-in facilities to set up your graph - to define the axis-scales and select which measured data and fitted values to plot.
37. **Graph of BQ Data:** Displayed **graph** of the selected **Bioassay Quantity**. The plotted values are selected in the **Graph Tool** - data points, fitted value for each data point (joined by blue lines), and/or the predicted bioassay quantity shown by the green curve.
38. **Bioassay Calculation Progress Indicator:** Indicates the calculation in progress, the proportion of each sequential task completed, and completion of the whole calculation. When the calculation is complete, the results are automatically displayed.
39. **OK Button:** Click to **save all current bioassay values** and **calculated results** in the currently open **Parameter File (*.ix)** - and return to the **Main Screen**.
40. **Bioassay Calculation Status Bar:** This shows (1) the **Indicator Nuclide**, (2) the set of **Radionuclide Bioassay Models** used, and (3) the **Fitting Method** used.

2.2.3. Visual Tour of the Table Tool

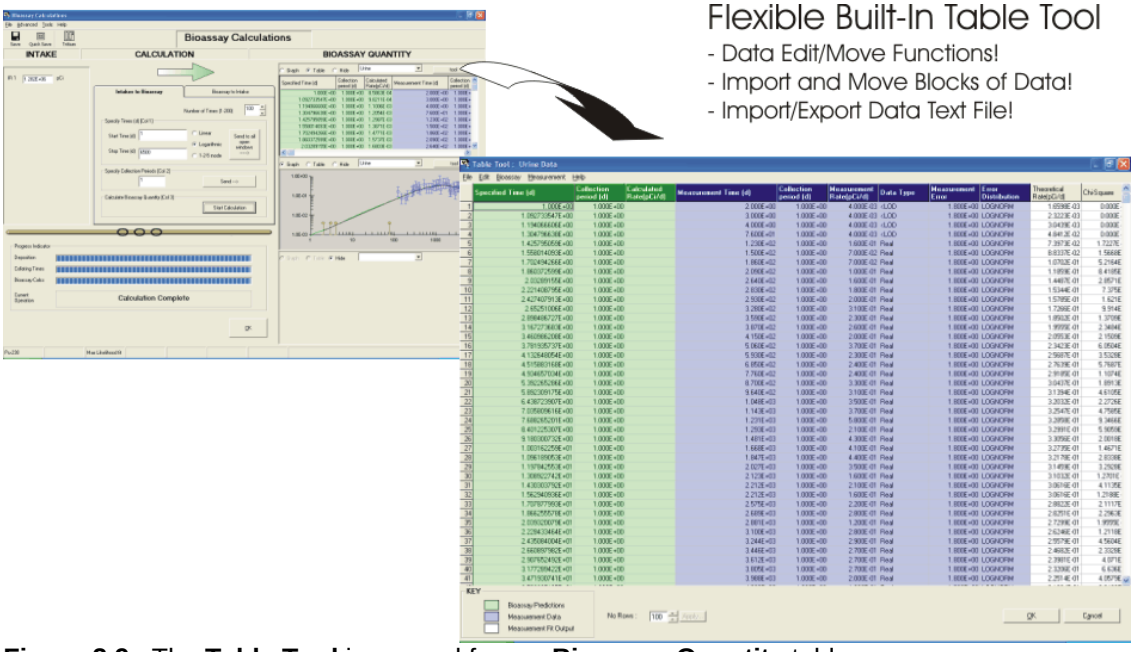


Figure 2.9. The **Table Tool** is opened from a **Bioassay Quantity** table.

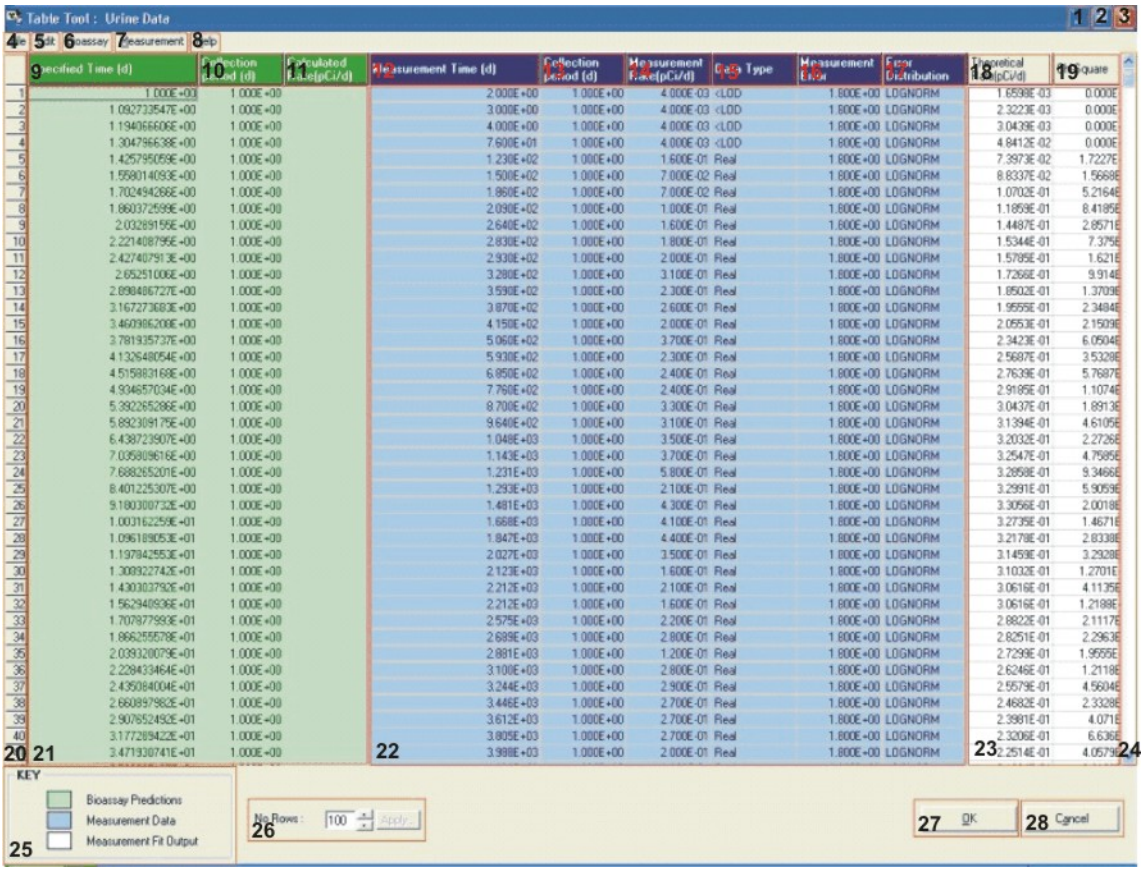


Figure 2.10. What's in the **Table Tool**?

Key to the Table Tool

1. **Minimize Table Tool:** You can't minimize this.
2. **Reduce Table Tool to a Window:** This reduces the **Table Tool** to a smaller (moveable) window - with the **Bioassay Calculations** screen in background.
3. **Exit Table Tool:** This exits the **Table Tool - without saving any recent changes of** parameter values to the **Parameter File** and **Bioassay Quantity** table - you will be warned!
4. **File Menu (Table Tool):** Click to (1) **Import an ASCII Data File**, or (2) **Exit the Table Tool** - you will be prompted to **Save** your changes. The ASCII data file can be (a) comma separated; (b) tab delimited; (c) space delimited, or (d) with your own defined delimiter. You will be guided by an intelligent **ASCII File Import Wizard** - which, for example, will let you view the data file before importing it and, if requested, will automatically open a sufficient number of rows in the **Table Tool** to receive the imported data.
5. **Edit Menu (Table Tool):** (1) **Cut**, (2) **Copy** or (3) **Paste** highlighted data; (4) **Insert** or (5) **Delete** a row of data; (6) **Delete Cell Contents**.
6. **Bioassay Prediction Menu:** (1) **Generate** a range of **Time** values (Linear, Logarithmic, or 1-2-5 Mode), (2) **Insert** or (3) **Delete** a row of predicted bioassay values.
7. **Generate Measurement Errors:** (1) **Uniform Absolute**, (2) **Uniform Relative**, or (3) **Square Root**.
8. **Table Tool Help Menu:** Open **HTML Help documentation**.
9. **Specified Time Column:** This column displays the **Time** (d) since the **Reference Date** - or the absolute **Date** (+ time-of-day in hh:mm) - for each predicted value of the **Bioassay Quantity**. These are the time-points plotted on the x-axis of the graph. Use the **Tool | Change Units to Time** toggle in the **Tool Menu** to change all **Time** values to **Date**.

10. **Collection Period (for Predicted BQ):** The hypothetical **Collection Period** is the same for all predicted **urinary** or **fecal** excretion amounts - usually 1 d. You can load this into all data rows with one click from the **Intakes to Bioassay Quantities** panel (**Bioassay Calculations** screen) - or simply **Paste** the required value into the whole **Collection Period** column in the **Table Tool**.
11. **Predicted BQ Value Column:** Clicking the **Start Calculation** button (**Intakes to Bioassay Quantities** panel) will calculate the **Bioassay Quantity** values for all defined time-points - and display the results automatically in Column 3. The column heading changes automatically with the selected **Bioassay Quantity**; either (1) **Calculated Rate** (Activity/d) for **urine** or **feces**, or (2) **Calculated Value** (Activity) for **other bioassay quantities**.
12. **Measurement Time Column:** This column displays the **Time** (d) since the **Reference Date** - or the absolute **Date** (+ time-of-day in hh:mm) - for each measured value (sample) of the **bioassay quantity**. These are the time-points plotted on the x-axis of the graph. Use the **Tool | Change Units to Time** toggle in the **Tool Menu** to change all **Time** values to **Date**.
13. **Collection Period (for Measured BQ):** The actual **Collection Period** (for **urine** or **fecal** samples) is entered (and displayed) in fractional-d. This can be different for each sample.
14. **Measured BQ Value Column:** The column heading changes automatically with the selected **Bioassay Quantity**; either (1) **Measurement Rate** (Activity/d) for **urine** or **feces**, or (2) **Measurement Value** (Activity) for **other Bioassay Quantities**. **NB:** All **urine** and **fecal** sample results **MUST** be entered as (normalized) **DAILY rates**, *i.e.,* Activity/d.
15. **Data Type Column:** This displays the **type** of each data point - either (1) **< LOD** (less than Limit of Detection); (2) **Real** (reliable measured value); or (3) **Imaginary** (unreliable measured value that will be ignored in the fitting procedure).
16. **Measurement Error Column:** This displays the value of the **measurement error** for each data point - plotted as a "**+/-**" bar in the graph.
17. **Error Distribution Column:** This displays the type of error distribution for each data point as (1) **Normal** or; (2) **Lognormal** - you can designate the error distribution as Normal for some data points and Lognormal for others, as appropriate.
18. **Theoretical BQ Value Column:** This displays the fitted **Bioassay Quantity** value for every sample. For **urine** and **feces**, this is the **fitted daily excretion rate** for the amount of excretion calculated for the **Collection Period** of each sample. For **other Bioassay Quantities**, this is simply the **fitted activity** at each measurement time.
19. **Chi-Square Column:** This shows the value of χ^2 - for each fitted value of the bioassay quantity.
20. **Row Numbers:** The number of rows displayed in the Table Toll depends on your screen resolution setting (*e.g.*, 36 rows for 1024 × 768 pixels). **N.B.:** the green and blue rows are filled independently - the number of filled **green** rows (time values) for the **predicted** bioassay values is independent of the number of filled **blue** rows (time values) for the **measured** bioassay data.
21. **Predicted BQ Values Table:** Columns 1-3 (with **green** background) display the **predicted Bioassay Quantity** values - with up to 200 rows, 1 row per data point (time value). These data are plotted as a **green curve** in the associated graph.
22. **Measured BQ Data Table:** Columns 4-9 (with **blue** background) display the **measured Bioassay Quantity** values (up to 200 rows, 1 row per data point). The measured values are plotted as **blue symbols** in the associated graph.
23. **Data Fit Table:** In the associated **graph**, the **fitted Bioassay Quantity** values (for each measured data point) are joined by a series of **blue lines**.
24. **Row-Scroll Bar (Table Tool):** Use this to view **hidden rows**, *i.e.,* additional data rows below those displayed.
25. **Color Key:** (1) Predicted values have a Green background; (2) Measured values have a Blue background; (3) Fitted values have a White background.

26. **Set Number of Rows:** Use this dialog box to **open** the **entered number of rows** in the whole **Table Tool** (Columns 1-10), or to **append** rows to those already opened.
27. **Table OK Button:** Click to **save all changes** made in the **Table Tool** - and **close** the **Table Tool**. This will return you to the **Bioassay Calculations** screen - where the associated **Table** in a **Bioassay Quantity** window will automatically be updated.
28. **Table Cancel Button:** Click to **cancel all changes** made in the **Table Tool** since these were last saved - and **close** the **Table Tool**. This will return you to the **Bioassay Calculations** screen - where the associated **Table** in a **Bioassay Quantity** window will not be changed.

2.2.4. Visual Tour of the Graph Tool

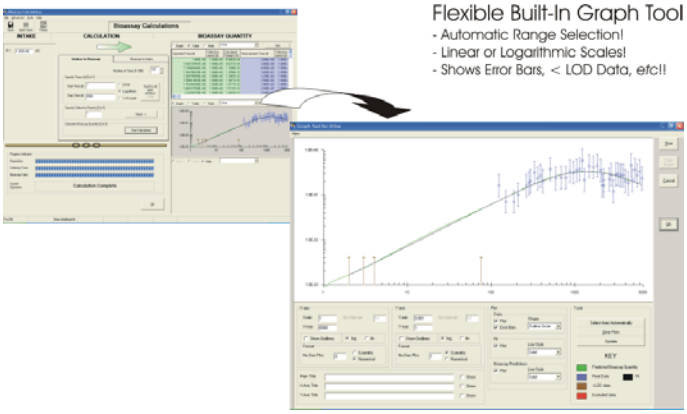


Figure 2.11. The **Graph Tool** is opened from a **Bioassay Quantity** table.

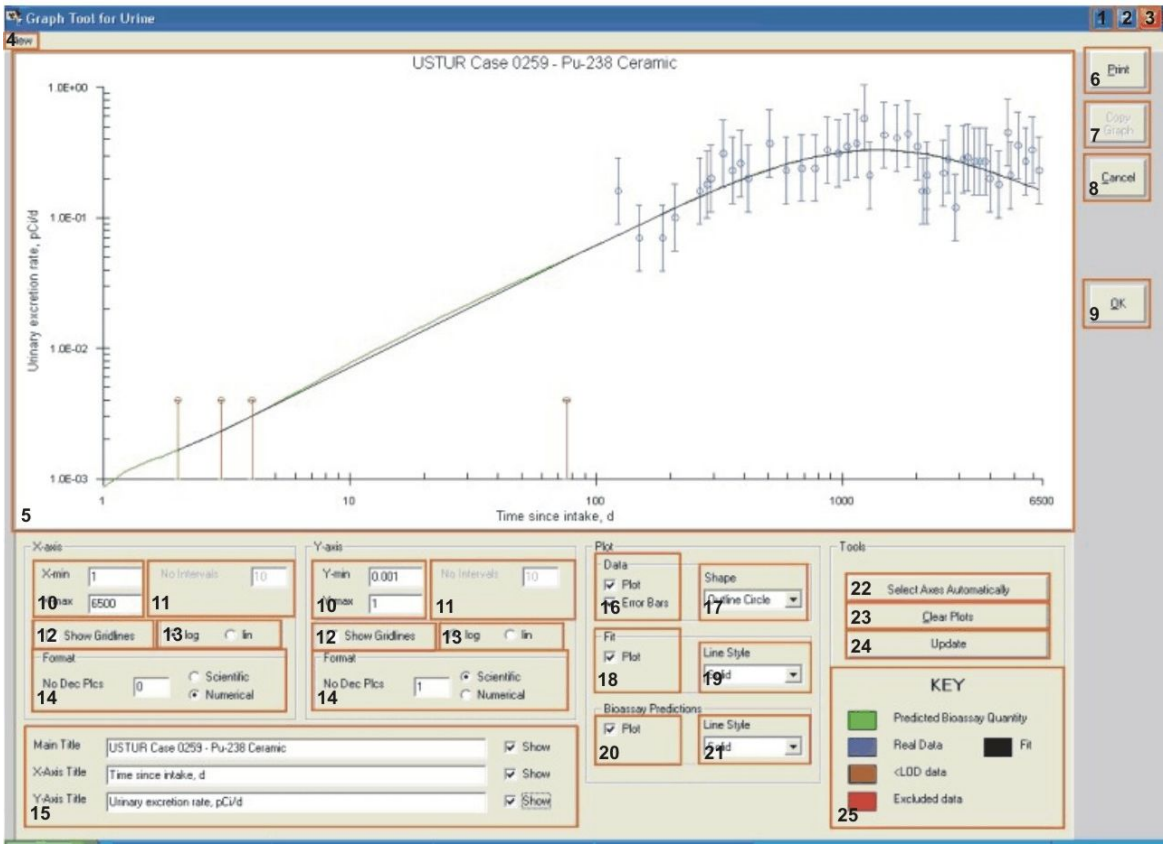


Figure 2.12. What's in the **Graph Tool**?

Key to the Graph Tool

1. **Minimize Graph Tool:** You can't minimize this.
2. **Reduce Graph Tool Size:** This reduces the **Graph Tool** to a smaller (moveable) window - with the **Bioassay Calculations** screen in background.
3. **Exit Graph Tool:** This exits the **Graph Tool** - without saving any recent changes to the graph settings.
4. **Graph View:** Select to **Maximize** the displayed size of the **Graph** - don't show graph control functions.
5. **Displayed Graph:** This example shows (1) **Logarithmic x- and y-axes**; (2) measured **data points** with their **error bars** (plotted in **blue**); (3) **< LOD data points** plotted at the **Limit of Detection** (in **brown**); (4) the **fitted values** (joined by **blue lines**); (4) the **predicted bioassay quantity** curve (in **green**).
6. **Print Graph Image:** This sends an image of the whole **Graph Tool** screen to your designated Windows® printer.
7. **Copy Graph:** Reserved for future implementation.
8. **Cancel Changes:** This cancels any changes made to the graph since this was last saved.
9. **Graph OK Button:** This saves all **Graph** settings/updates and returns you to the **Bioassay Calculations** screen - where your graph will be displayed in the associated **Bioassay Quantity** window.
10. **Change Axes Ranges:** You can change the **minimum** and **maximum** values of the x- and y-axes. You will be warned if you try to select zero for the minimum value on a logarithmic scale.
11. **Number of Intervals:** Sets the number of **ticks** on the x- or y-axis (independently).
12. **Show Gridlines:** Check the box to toggle on/off the gridlines for each axis (independently).
13. **Linear or Logarithmic Scales:** Select either a linear or a logarithmic scale for the x- and y-axis (independently). You will be warned if you select a logarithmic axis scale for a data set that contains a zero value of that parameter.
14. **Format Axis Scales:** (1) Select the number of digits you require to be displayed after the decimal point; (2) Select to switch the axis scales between **Numerical** and **Scientific** notation.
15. **Graph and Axes Titles:** Enter your **Titles**, and check the associated box to show each Title on the graph. The **Show** checkbox toggles on/off each **Title** independently - without having to click the **Update** button.
16. **Plot Data Checkboxes:** Check (1) **Plot** - plots data only, or; (2) **Plot + Error Bars** - plots error bars (if data are already plotted).
17. **Plot Fit Checkbox:** Check this to plot the **fitted values** (for each data point). Sequential fitted values are joined by straight lines (in **black**).
18. **Select Data Symbol:** Select the **data symbol** from the drop-down list. To change the data symbol you need to select the new symbol and then click the **Update** button.
19. **Fit Line Style:** Select from the drop-down list the **style** of the **lines** used to join the **fitted data points**. To change the line style you need to select the new style and then click the **Update** button.
20. **Plot Predicted Bioassay Values:** Check the box to plot the **predicted bioassay values**. These are joined sequentially by straight lines (in **green**). You can choose the number of predicted points in order to produce a pseudo-continuous curve (with fine time-resolution).
21. **Prediction Line Style:** Select from the drop-down list the **style** of the **lines** used to join the **predicted bioassay values**. To change the line style you need to select the new style and then click the **Update** button.
22. **Select Axes Automatically:** This detects the ranges of x- and y-values in your data set, and scales the axes accordingly.

23. **Clear Plots:** This **clears all plotted data** from the displayed graph - but not the axis scales, plot settings, or titles. You can **restore** the plot instantly by clicking the **Update** button.
24. **Update Button:** This **updates the graph** with any settings that you have changed - and re-plots the data.
25. **Graph Key:** This shows the colors used to represent the **various types of data**.

2.3. Dose Calculations Screen

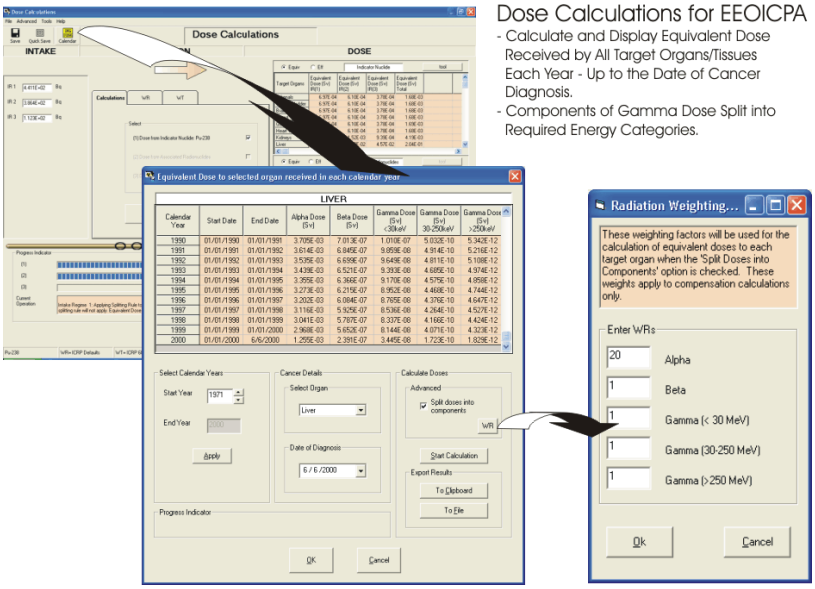

Dose Calculations for EEOICPA
- Calculate and Display Equivalent Dose Received by All Target Organs/Tissues Each Year - Up to the Date of Cancer Diagnosis.
- Components of Gamma Dose Split into Required Energy Categories.
Dose Calculations
INTAKE
DOSE
Equivalent Dose to selected organ received in each calendar year
LIVER
Radiation Weighting...
These weighting factors will be used for the calculation of equivalent doses to each target organ when the 'Split Doses into Components' option is checked. These weights apply to compensation calculations only.
Enter WRs
20
Alpha
1
Beta
1
Gamma (< 30 MeV)
1
Gamma (30-250 MeV)
1
Gamma (>250 MeV)
Ok
Cancel

Figure 2.13. The **Dose Calculations** screen.

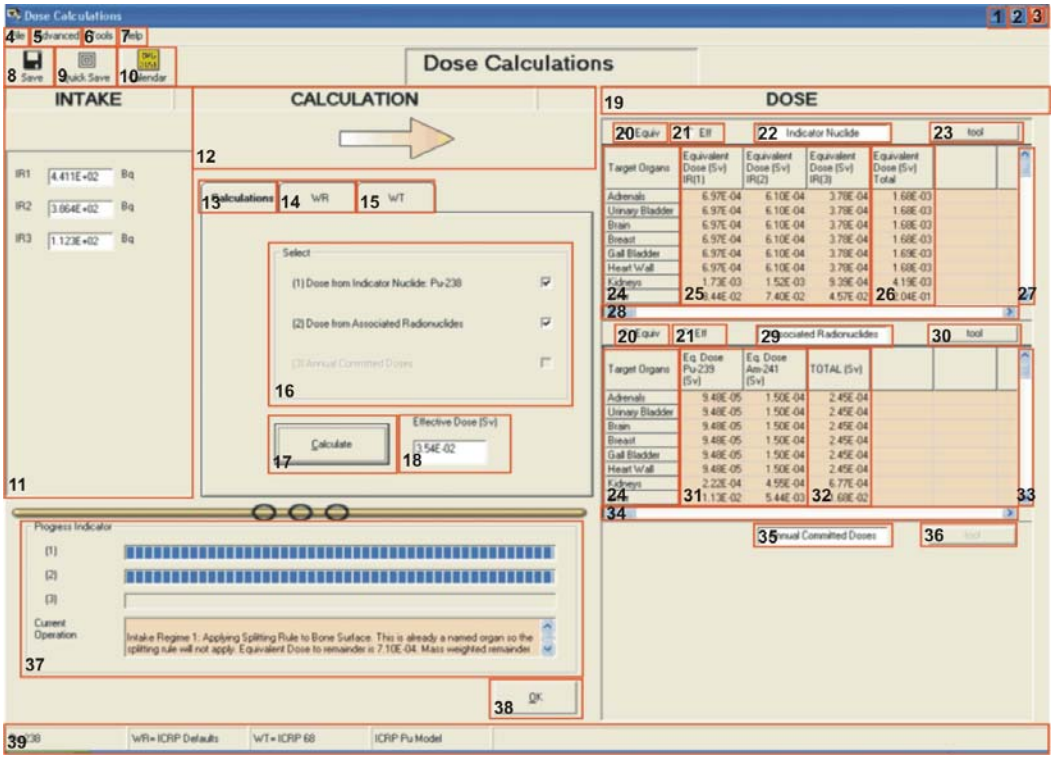


Figure 2.14. What's in the **Dose Calculations Screen**?

Key to the Dose Calculations Screen

1. **Minimize Dose Calculations Screen:** Not used.
2. **Reduce Dose Calculations Screen:** This reduces the size of the **Dose Calculations** screen to a window - visible on top of the **Main Screen**.
3. **Exit Dose Calculations:** This exits the **Dose Calculations** screen - without saving the most recently calculated results - and returns you to the **Main Screen**.
4. **Dose File Menu:** Select (1) **Save** - save the calculated doses in the current **Parameter.ix** file; (2) **Save As** - save the calculated doses in a custom-named Parameter File; (3) **Print** - print a screen-shot of the displayed **Dose Calculations** screen.
5. **Dose Tools Menu:** Not used in OCAS/ORAU-Edition (Version 4).
6. **Advanced Dose Menu:** Select **Advanced Dosimetry Options** - (1) **Dose** - **Include** (default) or **Exclude nuclear recoil energy** in SEEs for alpha emissions; (2) **Fitting** - select **Least Squares** method, **Maximum Likelihood** method (default), or *Bayesian Inference* method; (3) **Bioassay** - enable measurements of ^{241}**Am activity in the lungs** to be used to estimate an intake of ^{241}**Pu**; (4) **Miscellaneous** - allow intakes to be specified in mg (**Mass**).
7. **Help Menu (Dose):** Same options as **Help Menu** in **Main Screen** - (1) View **HTML Documentation**; (2) View **About IMBA Expert™ OCAS-Edition (Phase II)**; (3) View **Conditions of Use**; (4) Select **Help Mode**; (5) View **Quick Start Guide**.
8. **Save Icon (Dose):** Click to open the **Save As** dialog box - to save the calculated dose results (and all parameter information) in a named **Parameter File**.
9. **Quick Save Icon (Dose):** Click to Save the calculated dose results (and all parameter information) under the default **Parameters.ix** filename.
10. **ORG DOSE Calendar Button:** Click this to open the special window to calculate the "**Equivalent Dose to selected organ received in each calendar year**" – for output to the **I**nteractive **R**adio**E**pidemiology **P**rogram (**IREP**).
11. **Intake Panel (Dose):** This displays the amount of each **Intake** (up to 10 intakes) that is calculated from the **bioassay data** - or entered in the **Main Screen** - or directly in these dialog boxes.
12. **Direction of Calculation:** This always goes from **Intake** to **Dose**. The white/**tan** arrow signifies that the resulting doses are PREDICTED values (*c.f.,* the white/green arrow used to signify the **Intakes to Bioassay Quantities** prediction).
13. **Calculations Tab:** This displays the sub-panel for selecting the type of **Dose Calculation** (as shown here).
14. **WR Tab:** This allows you to select the **radiation weighting factors** that will be used in the calculation of **equivalent doses**, either (1) **ICRP-recommended values**, or; (2) your own **User Defined values**.
15. **WT Tab:** This allows you to select the **tissue weighting factors** and **remainder tissue rules** that will be used in the calculation of **effective doses**, (1) **10-CFR-835** values (for regulatory use); (2) **ICRP Publications 26/30** values; (3) **ICRP Publications 60/68** values; (4) your own **User Defined values**.
16. **Select Calculations:** Check the associated box to calculate (1) the **Committed Dose** from the **Indicator Nuclide**, and/or (2) the **Committed Dose** from **Associated Radionuclides**. You can perform all calculations in one step (by checking all three boxes). You will be warned if you have not yet defined the Biokinetic Model to be used for the Indicator Nuclide. For each Associated Radionuclide, the ICRP-recommended Biokinetic Model is loaded automatically.
17. **Calculate Dose Button:** Click this to perform the **selected dose calculation(s)**.
18. **Resulting Effective Dose:** This is displayed here - in your **selected Unit**.
19. **Dose Panel:** This displays all of the **calculated dose values**.
20. **Display Equivalent Doses:** Select this option to display all calculated values of **Equivalent Dose**. You can **switch** the display instantly to **Effective Dose**.
21. **Display Effective Doses:** Select this option to display all calculated values of **Effective Dose**. You can **switch** the display instantly to **Equivalent Dose**.

22. **Indicator Nuclide Doses:** The window below tabulates either (1) the **Committed Equivalent Dose** to each **Target Organ** that results from each **Intake Regime** (up to 10 IRs), or (2) the contributions to **Effective Dose** for each **Designated Organ** that result from each **Intake Regime** (up to 10 IRs) and the **Total Effective Dose** for each **Designated Organ** from the **Indicator Radionuclide**.
23. **Dose Tool (Indicator Nuclide):** Opens a full-screen table display of the calculated **equivalent** or **effective** doses (selectable) from intake(s) of the **Indicator Nuclide**.
24. **Target Organs:** List of **Target Organs** considered by ICRP in the assessment of **Effective Dose**.
25. **IR Dose Columns:** These columns display either (1) the calculated **Committed Equivalent Doses** to **Target Organs**, or; (2) the calculated **Effective Doses** to **Designated Target Organs**, **Remainder Tissues**, and the total **Effective Dose** - for **each Intake Regime** (IR).
26. **Total IR Dose Column:** This column displays either (1) the total calculated **Committed Equivalent Doses** to **Target Organs**, or; (2) the total calculated **Effective Doses** to **Designated Target Organs** and **Remainder Tissues**, and the overall **Effective Dose** - summed for all **Intake Regimes** (IRs).
27. **Organ Dose Scroll Bar:** Scroll to display doses to **additional target organs**, and/or the **total effective dose** (from each IR).
28. **IR Dose Scroll Bar:** Scroll to display doses resulting from **additional Intake Regimes**.
29. **Associated Radionuclide Doses:** The window below tabulates either (1) the **Committed Equivalent Dose** to each **Target Organ** that results from each **Associated Radionuclide** (up to 30 ARs) **summed for all IRs**, or (2) the contributions to **Effective Dose** for each **Designated Organ** that result from each **Associated Radionuclide** (up to 30 ARs) **summed for all IRs**, and the **Total Effective Dose** for each **Designated Organ** from all **Associated Radionuclides**.
30. **Dose Tool (Associated Radionuclides):** Opens a full-screen display of the calculated **equivalent** or **effective** doses (selectable) from intake(s) of **Associated Radionuclides**.
31. **AR Dose Columns:** These columns display either (1) the calculated **Committed Equivalent Doses** to **Target Organs**, or; (2) the calculated **Effective Doses** to **Designated Target Organs**, **Remainder Tissues**, and the **total Effective Dose** - for each Associated Radionuclide (AR).
32. **Total AR Dose Column:** This column displays either (1) the total calculated **Committed Equivalent Doses** to **Target Organs**, or; (2) the total calculated **Effective Doses** to **Designated Target Organs** and **Remainder Tissues**, and the **overall Effective Dose** - summed for all Associated Radionuclides (ARs).
33. **Organ Dose Scroll Bar (AR Doses):** Scroll to display doses to **additional target organs**, and/or the **total effective dose** (from each Associated Radionuclide).
34. **Dose Scroll Bar (AR):** Scroll to display doses resulting from additional Associated Radionuclides.
35. **Annual Committed Doses (OCAS):** This is not used in OCAS/ORAU-Edition.
36. **Dose Tool (Annual Committed Doses):** This is not used in OCAS/ORAU-Edition.
37. **Dose Progress Indicator:** This indicates progress through each step of the dose calculation(s) - separately for the **Indicator Nuclide** and any **Associated Radionuclides**. The "Current Operation" text box shows the calculation step being performed.
38. **Dose OK Button:** This **saves** all calculated dose values (in the current **Parameter File**) and returns you to the **Main Screen**.
39. **Dose Calculation Status Bar:** This shows (1) the **Indicator Nuclide**; (2) the **Radiation Weighting Factors** used; (3) the **Tissue Weighting Factors** used; (4) the set of **Indicator Nuclide Biokinetic Model** used.

2.3.1. The 'IREP Doses' Window

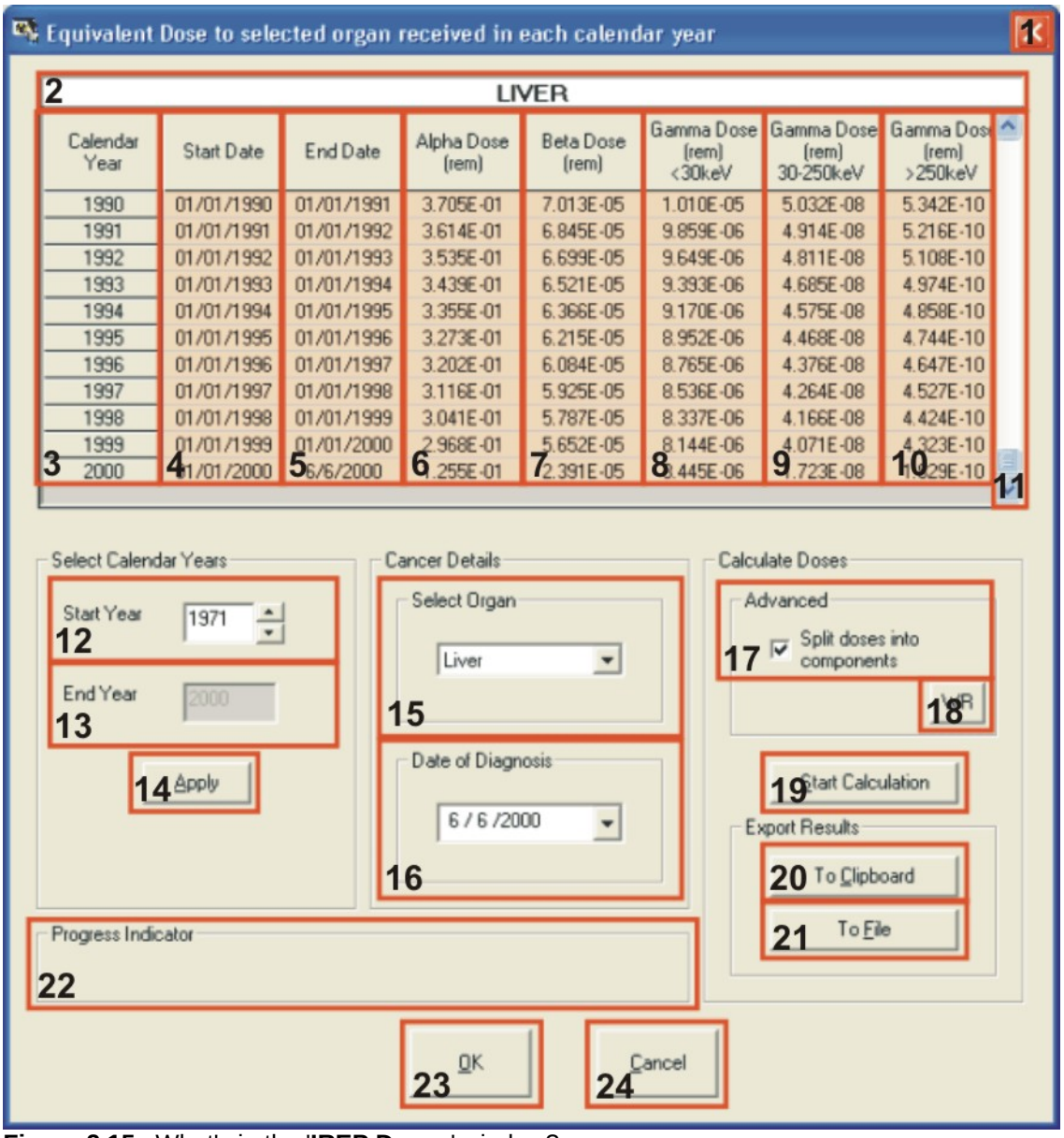


Figure 2.15. What's in the '**IREP Doses**' window?

Key to the 'IREP Doses' Window

1. **Exit 'IREP Doses' Window:** This exits the '**IREP Doses**' window – without saving the most recent calculated results – and returns you to the **Dose Calculations** screen.
2. **Selected Target Organ:** Target organ (or tissue) selected for display of equivalent doses received in listed calendar years.
3. **Calendar Year:** List of calendar years – from start of occupational exposure through date of cancer diagnosis. **Note:** In IMBA Expert™ OCAS/ORAU-Edition (Version 4.0), the maximum sequence is 50 years.
4. **Start Date:** Runs from January 1st (00.00) of the first year of occupational exposure through January 1st (00.00) of the year of cancer diagnosis.

5. **End Date:** Runs from December 31st (24.00) of the first year of occupational exposure through the date of cancer diagnosis.
6. **Alpha Dose:** Total **equivalent dose** from **alpha** emissions (of **Indicator Nuclide** and any radioactive progeny) **received** in the listed calendar year. A radiation weighting factor of **20** is applied automatically (unless changed manually – see **Advanced** option).
7. **Beta Dose:** Total **equivalent dose** from **beta** emissions (of **Indicator Nuclide** and any radioactive progeny) **received** in the listed calendar year. A radiation weighting factor of **1** is applied automatically (unless changed manually – see **Advanced** option).
8. **Gamma Dose (Low Energy):** Total **equivalent dose** from **gamma** emissions of emitted energy < 30 keV **received** in the listed calendar year (of **Indicator Nuclide** and any radioactive progeny). A radiation weighting factor of **1** is applied automatically (unless changed manually – see **Advanced** option).
9. **Gamma Dose (Intermediate Energy):** Total **equivalent dose** from **gamma** emissions of emitted energy between 30 keV and 250 keV **received** in the listed calendar year (of **Indicator Nuclide** and any radioactive progeny). A radiation weighting factor of **1** is applied automatically (unless changed manually – see **Advanced** option).
10. **Gamma Dose (High Energy):** Total **equivalent dose** from **gamma** emissions of emitted energy > 250 keV **received** in the listed calendar year (of **Indicator Nuclide** and any radioactive progeny). A radiation weighting factor of **1** is applied automatically (unless changed manually – see **Advanced** option).
11. **Calendar Year Scroll Bar:** Use to scroll through all years of occupational exposure – up to the date of cancer diagnosis.
12. **Start Year:** Enter the **Year** when the occupational exposure first started. The 'default' (pre-loaded) value is 1980. IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) allows you to specify a **Start Year** up to **50 years** before the **End Year** (year of cancer diagnosis).
13. **End Year:** Runs from January 1st (00.00) in the **year of cancer diagnosis** through the **date of cancer diagnosis**.
14. **Apply Start Year:** Clicking the '**Apply**' button **saves** the entered value of '**Start Year**' in the **Parameter file**.
15. **Select Organ:** Select the **Target Organ** (or tissue) for which the calculated **annual equivalent doses** will be displayed – and written to the **output report** file (***.rpt**).
16. **Date of Diagnosis:** This is the date on which the **claimant's cancer** (of the **specified Organ**) was diagnosed.
17. **Split Dose Option:** Check this box to **split** the **annual equivalent doses** from **gamma** emissions into 3 ranges of emitted energy (**as required by NIOSH**).
18. **WR Button:** This is activated ONLY when the option to '**Split dose into components**' is selected. It **displays** the **radiation weighting factors** applied to calculate the equivalent doses received from alpha, beta and gamma emissions.
19. **Start Calculation:** Click to start calculation of the **equivalent doses received** in each or the specified calendar years.
20. **Export to Clipboard:** This copies the **table of calculated annual equivalent doses** to the Windows® clipboard – for pasting into a spreadsheet (or any other Windows® software application).
21. **Export to File:** This enables you to produce a "***.rpt**" file in the precise format required by MJW's '**FeedIREP**' software.
22. **Progress Indicator:** This shows the progress of the calculation of **equivalent doses** received in each of the **specified calendar years** (for a maximum of 50 years).
23. **OK Button:** Click to **save all calculated results** in the currently open **Parameter File** (***.ix**) – and return to the **Dose Calculations** screen.
24. **Cancel Button:** Click to return to the **Dose Calculations** screen **without saving** calculated results or most recent changes to the **Parameter file**.

3. How to Use the Main Screen

The ***Main Screen*** (opening screen) appears when you *click* the **IMBA Expert (ORAU)** icon - which runs **IMBA.exe**. This screen is shown in Figure 3.1.

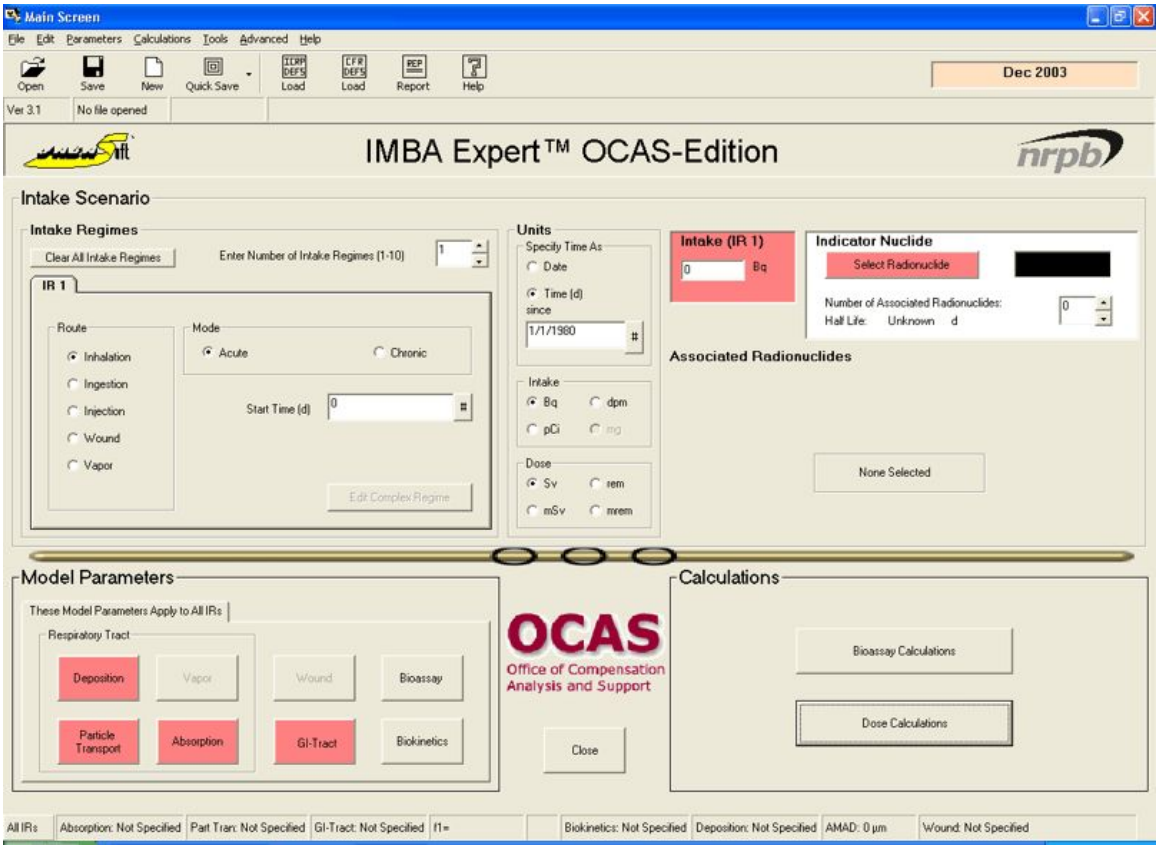


Figure 3.1. The **Main Screen** (opening screen).

The screen is divided into the following functional parts:

Top rows

- ***Menu Bar***.
- ***Short-cut Icons***.
- ***Parameter File Bar*** .

Top main panel

- ***Intake Scenario*** – subdivided into;
  1. **Intake Regimes (IR)** sub-panel – left side
  2. **Units** sub-panel – center
  3. **Radionuclide(s)** [by IR#] – right side.

Bottom main panel

- ***Model Parameters and Calculations*** – subdivided into;
  1. **Model Parameters** sub-panel – left side
  2. **Calculations** sub-panel – right side.

Bottom row

- ***Status Bar***.

3.1. Main Menus

The **Menu Bar**, shown at the top-left of the main window, gives the following options:

- **File** menu.
- **Edit** menu.
- **Parameters** menu.
- **Calculations** menu.
- **Tools** menu.
- **Advanced** menu.
- **Help** menu.

3.1.1. File Menu

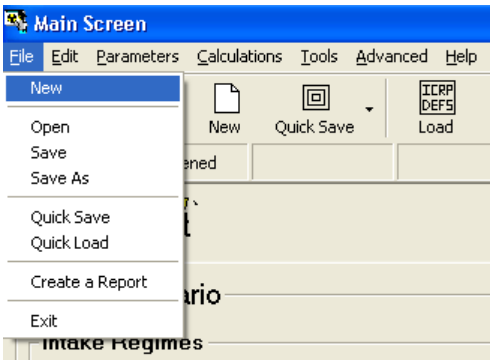


Figure 3.2. Drop-down **File** list box.

The **File** options are as follows:

- **New –** *Re-load* (and reset) IMBA Expert™ OCAS/ORAU-Edition for a new case study - with a *blank* parameter file.
- **Open – *Open*** any parameter file **"*.ix"** from the Folder [Install Drive:]\JABASOFT\IMBAEXUS\UserData\ (Figure 3.3), or browse to another Folder.
- **Save –** *Save* the current parameter set to the same **"*.ix"** filename.
- **Save As –** Allows you to define a new name for the **"*.ix"** file (appearance of dialog box is identical to Figure 3.3, but with **Save** button).
- **Quick Save –** *Save* the current set of parameter values (and calculated results) to the default parameter file "**parameters.ix**" in the Folder [Install Drive:]\JABASOFT\IMBAEXUS\.
- **Quick Load –** *Re-load* the parameter values (and calculated results) from the default parameter file "**parameters.ix**" in the Folder [Install Drive:]\JABASOFT\IMBAEXUS.
- **Create a Report** - *Open* the "**Report**" window. This will guide you through the steps needed to generate and save a **Case Report**.

- **Exit** - *Unload* and *Exit* IMBA Expert™ OCAS/ORAU-Edition.

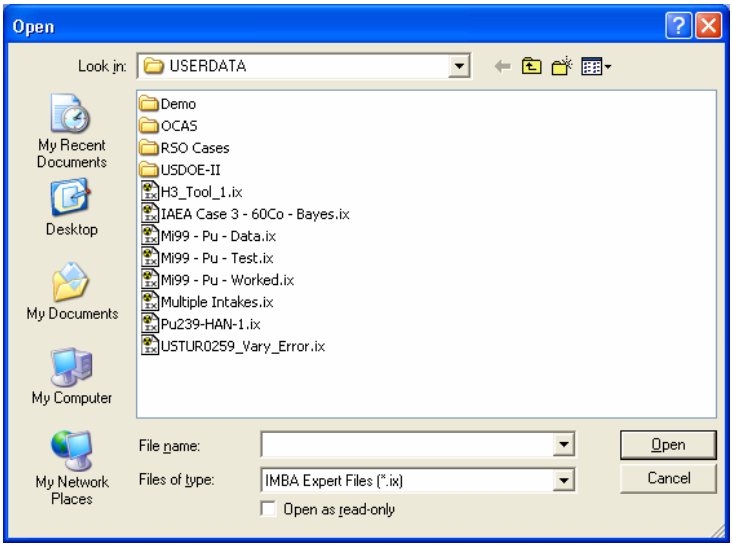


Figure 3.3. The **Open** parameter file dialog box.

3.1.2. Edit Menu

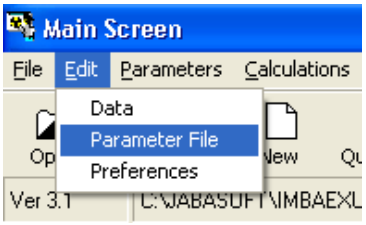


Figure 3.4. Drop-down **Edit** list box.

The **Edit** options are as follows:

- **Data** - *Open* the ***Bioassay Calculations*** screen in the "**Bioassay Quantity to Intake**" mode. This enables you to enter (or edit) **Bioassay Data** and/or perform **Intake** calculations.
- **Parameter File** - *Open* the named **Parameter File** in MS NotePad®. If no name has been specified, a blank Microsoft® Notepad file will be opened.
- **Preferences** - *Choose* (1) to play the "theme tune" at start-up - or keep the default setting (silence); (2) to automatically check the web for updates to IMBA Expert™ OCAS/ORAU-Edition - or keep the default setting (NO); (3) to 'Display all [execution] error messages' (default setting) and/or 'Display all warnings' (including all data checks performed automatically by the IMBA modules themselves).

Note: Only the ORAU Computer Operations Center (COC) **System Administrator** has '**Upgrade**' rights. In all installations of IMBA Expert™ OCAS/ORAU-Edition distributed to **Field Users** (Dose Assessors), the 'Upgrade' facility is **disabled**.

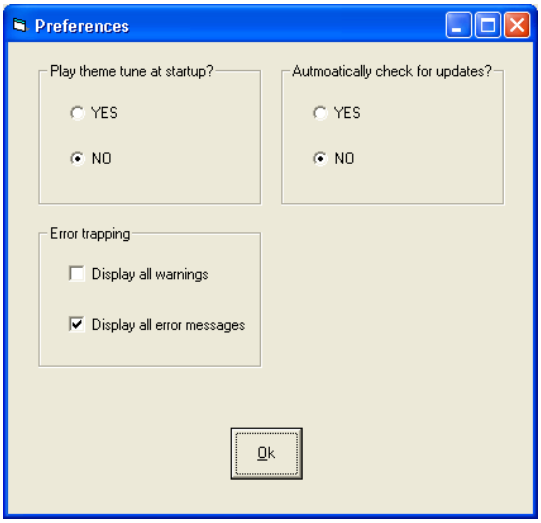


Figure 3.5. Start-up preferences.

3.1.3. Parameters Menu

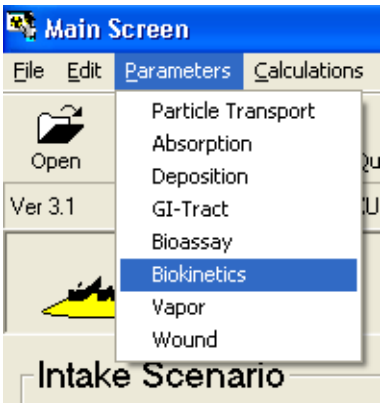


Figure 3.6. Drop-down **Parameters** list box.

The **Parameters** options are as follows:

- **Particle Transport** - *Open* the ***Particle Transport Model*** window. This enables you to *load* the values of **mechanical transport rates** recommended in *ICRP Publication 66* for the respiratory tract model - or define your own parameter values.

- **Absorption** - *Open* the ***Absorption Model*** window. This enables you to *load* the default values of **absorption rates** recommended in *ICRP Publication 66* for the **respiratory tract model** - or define your own parameter values.

- **Deposition** - *Open* the ***Deposition Model*** window. This enables you to *select* the default values of **aerosol size characteristics** recommended in *ICRP Publication 66* for the **respiratory tract model** (occupational exposure) - or define your own parameter values.

- **GI-Tract** - *Open* the ***GI Tract Model*** window. This enables you to *select* the default values of **transport rates between compartments** of the GI tract recommended in *ICRP Publication 30* - or define your own parameter values.

- **Bioassay** - *Open* the ***Bioassay Model*** window. This enables you to *select* the **bioassay function** for each bioassay quantity - either the function currently recommended by ICRP, or you can define your own function.

- **Biokinetics** - *Open* the ***Biokinetic Model*** window. This enables you to *select* the **retention function** for each source organ or tissue - either the function currently recommended by ICRP, or you can define your own function.

- **Vapor** - *Open* the ***Gases and Vapors Model*** window. This will enable you to *select* the default values recommended in *ICRP Publication 68* to represent occupational exposure to gases or vapors - or define your own parameter values.

- **Wound** - *Open* the ***Wound Model*** window. This will enable you to *select* the **wound retention function** - by default retention type, or you can define your own function.

3.1.4. Calculations Menu

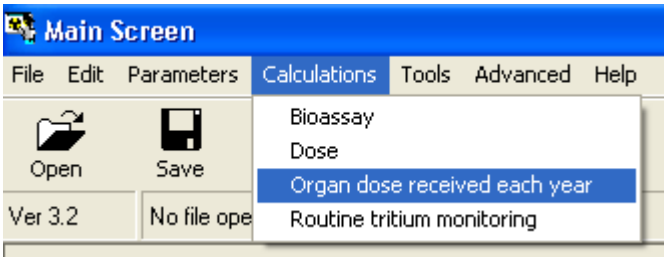


Figure 3.7. Drop-down **Calculations** list box.

The **Calculations** options are:

- **Bioassay** - *Open* the ***Bioassay Calculations*** screen in the "**Bioassay Quantity**" to "**Intake**" mode. This enables you to enter (or edit) **Bioassay Data** and/or perform Intake calculations.

- **Dose** - *Open* the ***Dose Calculations*** screen. This enables you to:

    1. *select* **radiation weighting factors**;
    2. *select* **tissue weighting factors**;
    3. *calculate* doses from the selected **Indicator Radionuclide**;
    4. *calculate* doses from any selected **Associated Radionuclides**.

- **Organ dose received each year** - implemented in IMBA Expert™ OCAS/ORAU-Edition to calculate annual equivalent doses received by a target organ or tissue, as required by NIOSH for input to the **I**nteractive **R**adio**E**pidemiological **P**rogram (NIOSH-**IREP**).

- **Routine tritium urinalysis** - *Open* a special calculator tool (Figure 3.8) to analyze routine tritium-in-urine monitoring data.

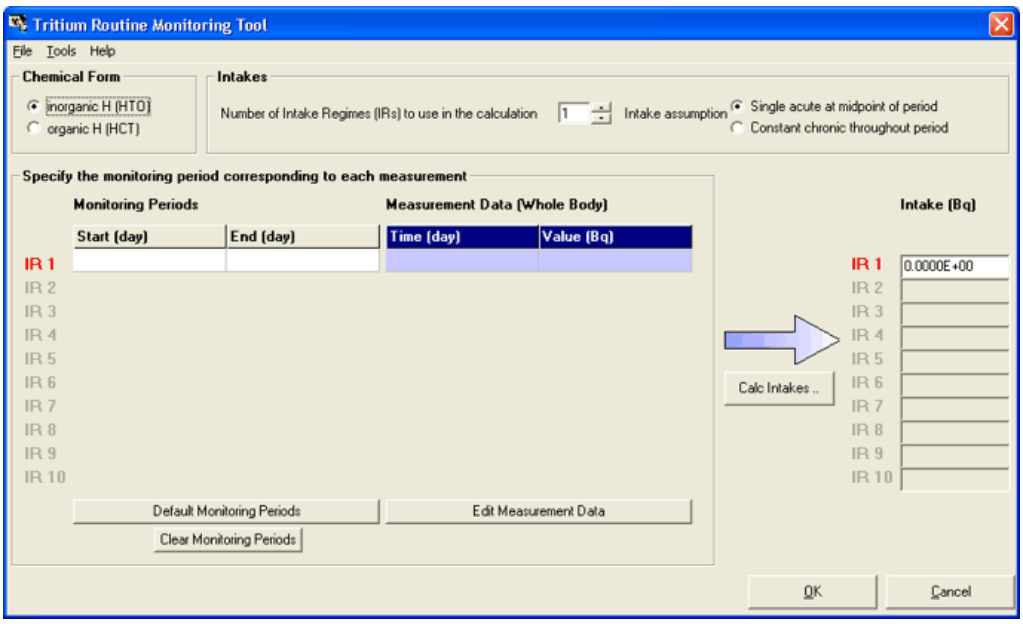


Figure 3.8. Calculator Tool for **routine tritium urinalysis**.

3.1.5. Tools Menu

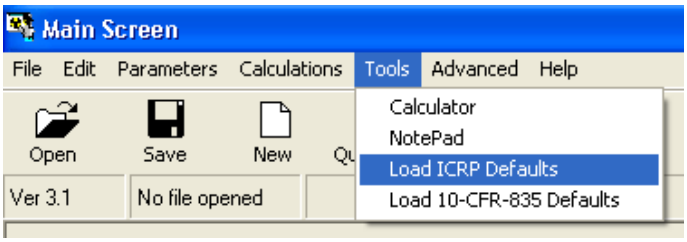


Figure 3.9. Drop-down **Tools** list box.

The **Tools** options are:

- **Calculator** - *Open* the Microsoft® ***Calculator*** window (Figure 3.10).
- **Notepad** - *Open* an "Untitled" Microsoft® ***NotePad File*** window.
- **Load ICRP Defaults** - *Open* automatically (in sequence):
    1. the ***F1 Values for ****** window - where "*******" is the pre-selected radionuclide - so you can *select* the appropriate value of the gut uptake fraction ($\mathbf{f_1}$) for the pre-selected radionuclide;
    2. the ***Bioassay Model*** window - this confirms that all currently recommended ICRP **bioassay functions** AND all other currently recommended ICRP models for the pre-selected radionuclide have been loaded.
- **Load 10-CFR-835 Defaults** - *Open* automatically (in sequence):
    1. the ***F1 Values for ****** window - where "*******" is the pre-selected radionuclide - so you can *select* the appropriate value of the **gut uptake fraction** ($\mathbf{f_1}$) for the pre-selected radionuclide;

2. the ***Bioassay Model*** window - this confirms that all currently recommended ICRP **bioassay functions** and **organ/tissue retention functions** for the pre-selected radionuclide have been loaded - BUT the loaded **tissue weighting factors** and **remainder tissue rules** are those prescribed in the **10-CFR-835 Regulation**.

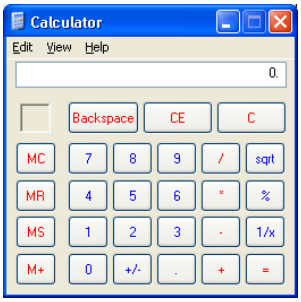


Figure 3.10. Microsoft® ***Calculator***.

3.1.6. Advanced Menu

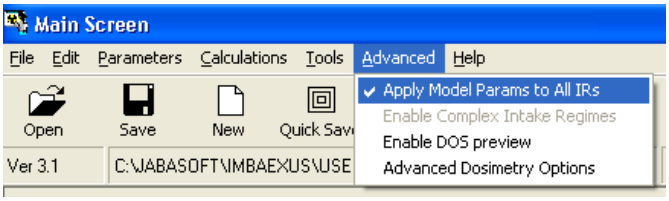


Figure 3.11. Drop-down **Advanced** list box.

The **Advanced** options are:

- **Apply Model Parameters to All IRs –** the **DEFAULT** option (**ticked**). This applies a **single set** of selected **model parameters** to **ALL *Intake Regimes***. **Disable** (un-tick) this default if you want to specify model parameters **individually** (and **independently**) for **every** intake regime.

- Enable **Complex Intake Regimes (reserved for future implementation)** - this will enable you to define specific patterns of intake over periods of time.

- **Enable DOS preview** - this is a "debugging" tool, used by the software's developers to examine the integrity of DOS input files produced by IMBA Expert™ in order to run the **IMBA** code modules.

- **Advanced Dosimetry Options** - opt to **Exclude** nuclear recoil energy from the SEEs for alpha emissions. For all IMBA Expert™ versions, the "default" is to **Include** nuclear recoil energy. OCAS/ORAU-Edition (Version 4) includes the following additional options:

    - **Fitting** - select the method (Figure 3.13) to be used to *fit bioassay data* (estimate intakes) from (1) Least Squares; (2) Maximum Likelihood; (3) Bayesian Inference.

    - **Bioassay** - select the special option to use **^{241}Am activity in lung** to estimate intake(s) of ^{241}Pu.

    - **Miscellaneous** - specify the bioassay quantity in **mass units (mg)**, *e.g.*, for urinalysis of uranium.

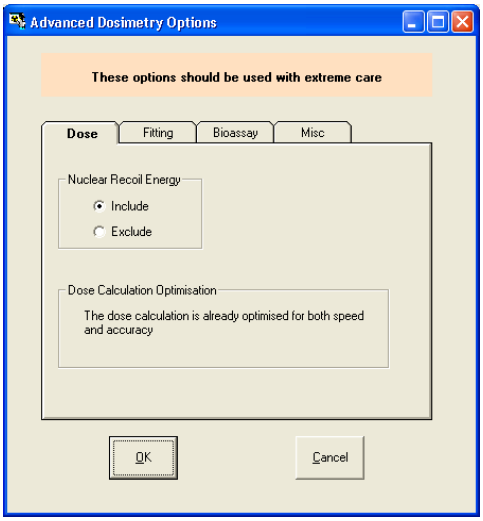


Figure 3.12. Tabs to select **Advanced Dosimetry Options**.

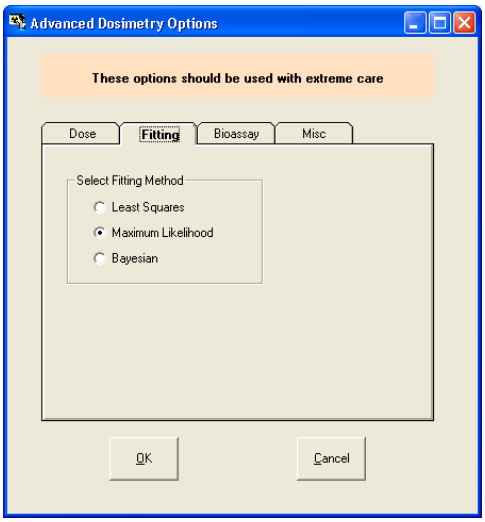


Figure 3.13. Options for **Fitting** bioassay data.

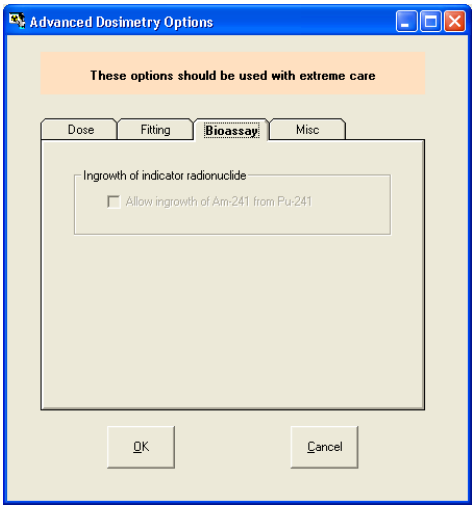


Figure 3.14. Special bioassay option for analyzing **^{241}Am ingrowth in the lungs** (from intake of ^{241}Pu).

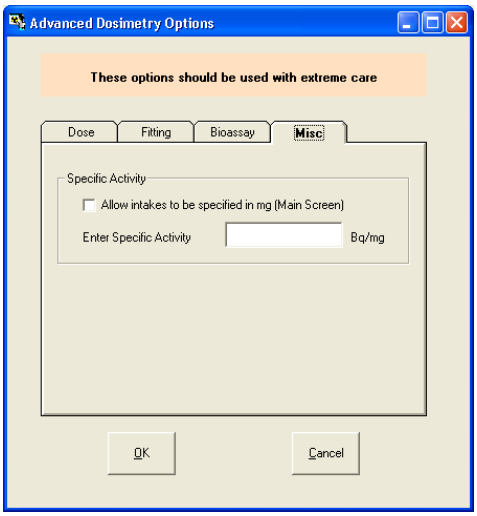


Figure 3.15. Miscellaneous option to use **mass units**.

3.1.7. Help Menu

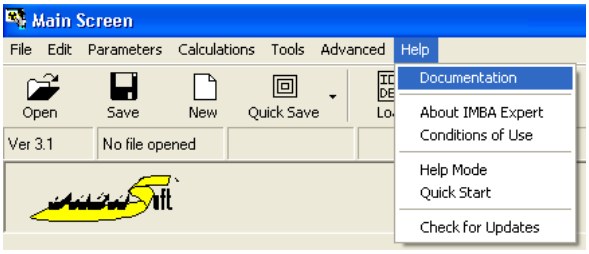


Figure 3.16. Drop-down **Help** list box.

The **Help** options are:

- **Documentation** - Show (this) **User Manual** and **Technical Basis** documentation.
- **About** IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) - Show **Authorship** and **Copyright Notice** (Figure 3.17).

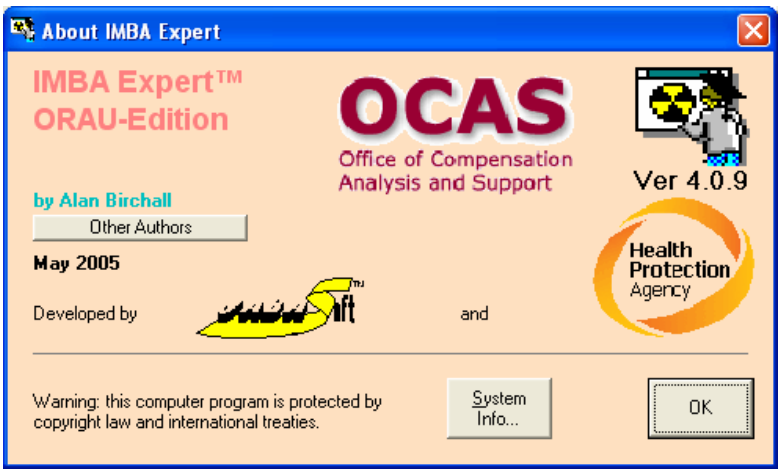


Figure 3.17. Authorship and Copyright Notice.

- **Conditions of Use** - Show **End-User License Agreement** ("**EULA**") for IMBA Expert™ OCAS/ORAU-Edition (Version 4.0).

Help Mode - Switch operation of IMBA Expert™ OCAS/ORAU-Edition from "**Run**" mode to special "**Mouse-over Help**" mode. In this special mode, a "**?**" appears next to your mouse pointer. When you move this over a screen control region, a brief message appears to explain the function of the control - see Figure 3.18 for the message that appears in ***Help Mode*** when your mouse pointer is over the **Tool Bar**. To exit ***Help Mode*** - and go back to the "**Run**" mode, you simply "**un-tick**" (disable) the ***Help Mode*** option (see Figure 3.19).

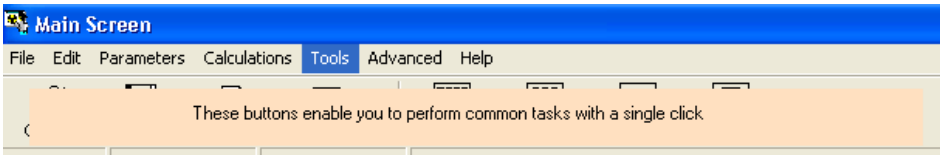


Figure 3.18. ***Help Mode*** message describing the function of the **Tool Bar**.

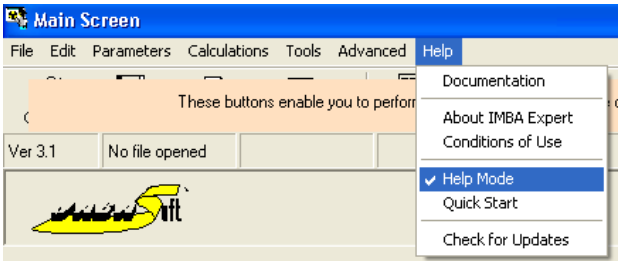


Figure 3.19. Re-click the ***Help Mode*** option to remove the **tick** (disable ***Help Mode***).

- **Quick Start** - *Opens* the scrollable ***Quick Start*** window (Figure 3.20). This contains a condensed description of the layout and operation of IMBA Expert™ OCAS/ORAU-Edition - to help you (as an experienced internal dosimetrist) get started more directly with using the software.

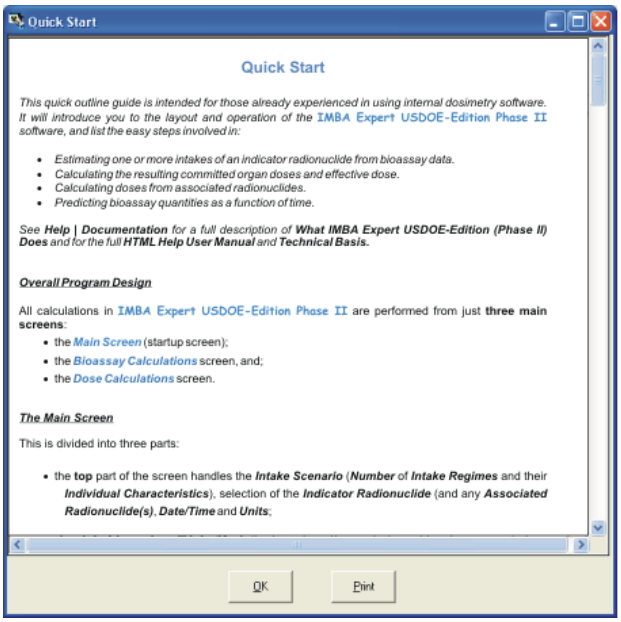

Quick Start
Quick Start
This quick outline guide is intended for those already experienced in using internal dosimetry software. It will introduce you to the layout and operation of the IMBA Expert USDOE-Edition Phase II software, and list the easy steps involved in:
Estimating one or more intakes of an indicator radionuclide from bioassay data.
Calculating the resulting committed organ doses and effective dose.
Calculating doses from associated radionuclides.
Predicting bioassay quantities as a function of time.
See Help | Documentation for a full description of What IMBA Expert USDOE-Edition (Phase II) Does and for the full HTML Help User Manual and Technical Basis.
Overall Program Design
All calculations in IMBA Expert USDOE-Edition Phase II are performed from just three main screens:
the Main Screen (startup screen);
the Bioassay Calculations screen, and;
the Dose Calculations screen.
The Main Screen
This is divided into three parts:
the top part of the screen handles the Intake Scenario (Number of Intake Regimes and their Individual Characteristics), selection of the Indicator Radionuclide (and any Associated Radionuclide(s), Date/Time and Units;
OK
Print

Figure 3.20. Scrollable ***Quick Start*** Help window.

- **Check for Updates** - **Available only to NIOSH/OCAS and authorized ORAU/MJW staff** - *Opens* the ***Updates Wizard*** (Figure 3.21). This automatically checks the web for available ***Updates*** to your IMBA Expert™ OCAS/ORAU-Edition software installation.

    - **If** your software is already ***Up-to-Date***, you will see the message shown in Figure 3.22.

    - **If not**, you will be guided through the process of *selecting* and *downloading* the available updated files. Any downloaded files will be installed automatically (Figures 3.21A-C) - and the ***Updated*** software will be ready to for you to continue using (Figure 3.22).

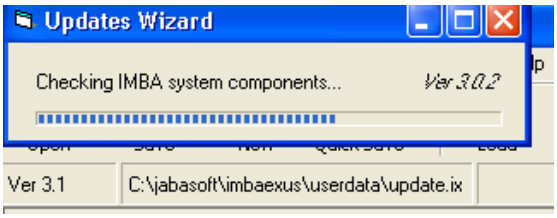


Fig 3.21A. Updates Wizard - Checking for Updates.

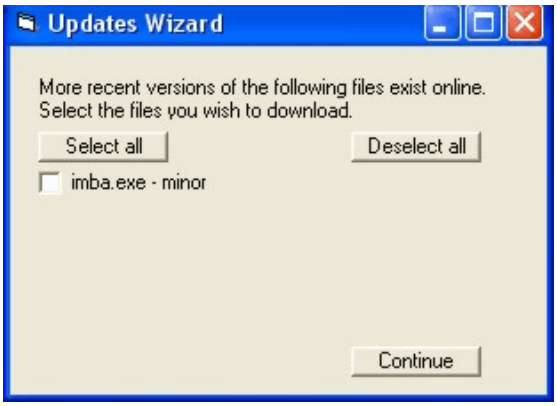


Fig. 3.21B. Updates Wizard - Available Updates.

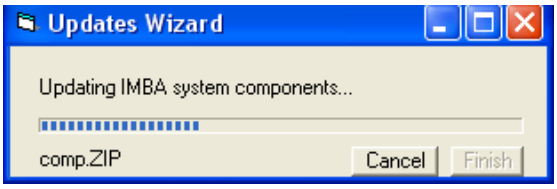


Fig. 3.21C. Updates Wizard - Update Progress Indicator.

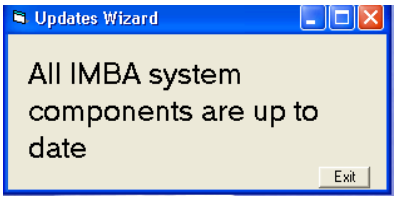
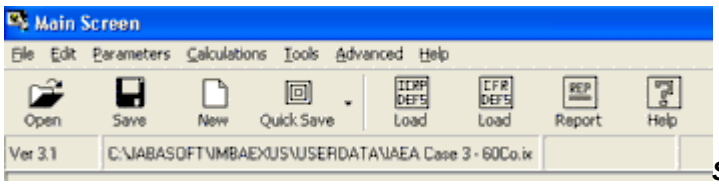
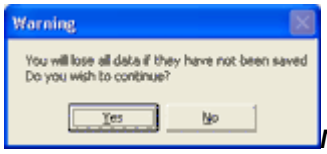
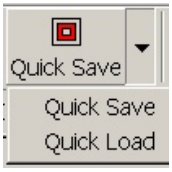


Fig. 3.22. Message displayed when system components are **up-to-date**.

3.2. Tool Buttons

The **Tool Bar**, shown at the top-left of the ***Main Screen***, just below the **Menu Bar**, contains **Tool Buttons** to let you perform common tasks with a **single click**. The tool buttons change appearance as the mouse pointer is passed over them.

	Open a **Parameter File "*.ix"** from the directory [Install Drive:]\JABASOFT\IMBAEXUS\ UserData\ - or browse to another folder.
	 ***Save*** the current parameter set to the **"*.ix" Filename** shown in the **"Parameter File"** box (top-right-corner of **Main Screen**). If no **Filename** is shown, the **Save** button opens the **Save As** dialog box (Figure 3.23).
	 ***New*** - clear all parameter values and case data and open a blank parameter file. This warning message will appear - to prevent you from accidentally losing unsaved data! If you click "**Yes**," the "**Parameter File**" box will display "**No file opened**."
	***Quick Save*** the parameter file [C:]\JABASOFT\IMBAEXUS**parameters.ix**. ***Quick Load*** the parameter file [C:]\JABASOFT\IMBAEXUS**parameters.ix**. If you installed IMBA Expert™ OCAS/ORAU-Edition (**IMBA.exe**) on a different drive, the **parameters.ix** file will automatically be saved to and reloaded from your installation drive.
	Load ICRP Defaults - *Quick-load* **ALL ICRP-recommended models** with minimum interaction from you. *Clicking* the *button* will *Open* automatically (in sequence): (1) the ***F1 Values for*** ******* window - where "*******" is the pre-selected radionuclide - so you can *select* the appropriate value of the **gut uptake fraction** ($\mathbf{f_1}$) for the pre-selected radionuclide; (2) the ***Bioassay Model*** window - to *confirm* that all currently recommended ICRP **bioassay functions** AND **all other currently recommended ICRP models** for the pre-selected radionuclide have been loaded.
	Load 10-CFR-835 Defaults - *Quick-load* **ALL ICRP-recommended models** with **10-CFR-835 prescribed tissue weighting factors**. *Clicking* the *button* will *Open* automatically (in sequence): (1) the ***F1 Values for*** ******* window - where "*******" is the pre-selected radionuclide - so you can *select* the appropriate value of the **gut uptake fraction** ($\mathbf{f_1}$) for the pre-selected radionuclide; (2) the ***Bioassay Model*** window - to *confirm* that all

	currently recommended ICRP **bioassay functions** and **organ/tissue retention functions** for the pre-selected radionuclide have been loaded - AND the loaded **tissue weighting factors** and **remainder tissue rules** are those prescribed in the **10-CFR-835 Regulation**.
	Report - *Open* the ***Report*** window to create a case report. This will be saved in Folder**filename** [Install Drive:]\JABASOFT\IMBAEXUS\UserData**Default.RPT** (or in the equivalent folder on your installation drive). Alternatively, you can **browse** to *save* your **Report** in any other **folder** and/or **filename** of your choice.
	Help - View a scrollable summary of available **Help Options** (Figure 3.24).

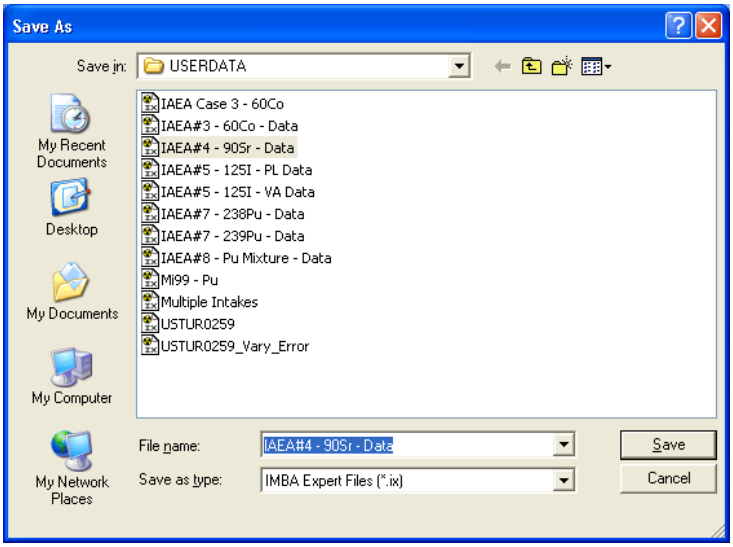


Figure 3.23. Save As dialog box.

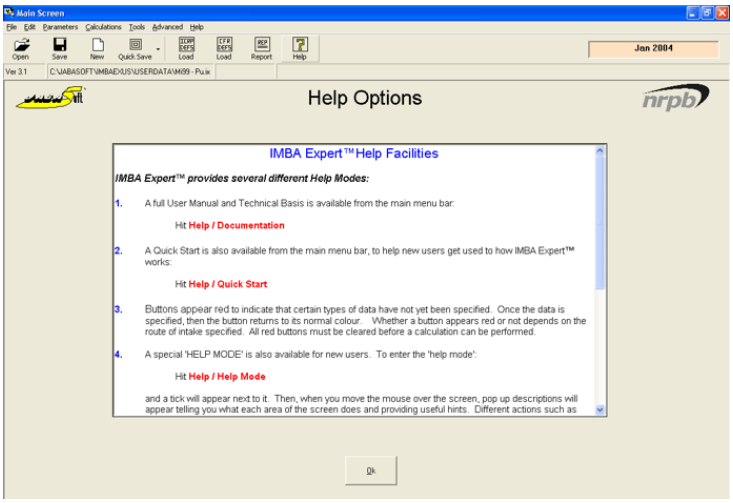

Main Screen
Jan 2004
Help Options
IMBA Expert™ Help Facilities
IMBA Expert™ provides several different Help Modes:
1. A full User Manual and Technical Basis is available from the main menu bar:
Hit Help / Documentation
2. A Quick Start is also available from the main menu bar, to help new users get used to how IMBA Expert™ works:
Hit Help / Quick Start
3. Buttons appear red to indicate that certain types of data have not yet been specified. Once the data is specified, then the button returns to its normal colour. Whether a button appears red or not depends on the route of intake specified. All red buttons must be cleared before a calculation can be performed.
4. A special 'HELP MODE' is also available for new users. To enter the 'help mode':
Hit Help / Help Mode
and a tick will appear next to it. Then, when you move the mouse over the screen, pop up descriptions will appear telling you what each area of the screen does and providing useful hints. Different actions such as
Ok

Figure 3.24. Summary of available **Help Options**.

3.3. Parameter File Bar

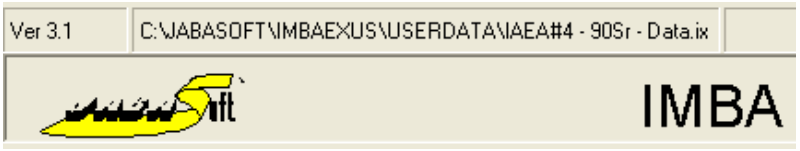


Figure 3.25. Parameter File bar.

- This shows the **Folder** where the current **Parameter File** ("***.ix**") was last *saved* - and its **filename**.

  The box to the left shows the **Version Number** of this software (**Vers. 3.2**).

Key Tip: You can load IMBA Expert™ OCAS/ORAU-Edition selected **Parameter File** automatically - simply by *double-clicking* on the **file icon**! See the **Quick Start** guide for instructions.

IAEA#3 - 60Co.ix

For example, *double-clicking* this "**IX**" icon (in the **UserData1\Demo** folder) will **Run** IMBA Expert™ OCAS/ORAU-Edition - with the **Parameter File** "IAEA#3 - 60Co.ix" already opened.

Note: If IMBA Expert™ OCAS/ORAU-Edition is already running, *double-clicking* on an "**IX**" icon will load and run a second copy.

3.4. Main Status Bar

Figure 3.26. New Status Bar - appearance for **New** (blank) **Parameter File**.

The **Main Status Bar** is on the bottom row of the ***Main Screen***. When you ***select*** a **New** (blank) **Parameter File**, the **Main Status Bar** appears as shown in Figure 3.26. The items listed are:

- **All IRs** - indicates that all specified model parameters will apply to *ALL* **Intake Regimes** (the **default** setting).
- **Absorption** - respiratory tract absorption parameters initially *Not Specified*.
- **Part Tran** - respiratory tract particle transport parameters initially *Not Specified*.
- **GI-Tract** - gastrointestinal tract model parameters initially *Not Specified*.
- **f1** - gut absorption fraction initially *Blank*.
- **Biokinetics** - biokinetic model parameters initially *Not Specified*.
- **Deposition** - respiratory tract deposition model parameters initially *Not Specified*.
- **AMAD** - activity median aerodynamic diameter (and other aerosol size parameters) initially *Not Specified*.
- **Wound** - wound model parameters initially *Not Specified*.

Figure 3.27 shows the **Main Status Bar** for a **Parameter File** in which all of the above items have been specified (except for the **Wound** model parameters). In this example, the **"All IRs"** label has been replaced with the **"IR 1"** label. This denotes that the parameter settings displayed on the **Main Status Bar** apply to **Intake Regime #1**. Up to **10 IRs** can be specified independently - and their parameter settings can each be displayed (one **IR** at-a-time) on the **Main Status Bar**.

Figure 3.27. Working Status Bar - appearance for **Working** (in-use) **Parameter File**.

3.5. Intake Scenario Panel

Figure 3.28. Intake Scenario panel.

The ***Intake Scenario*** panel holds the sub-panels for specification of:

- **Intake Regimes** - left side;
- **Units** - centre;
- **Intake Amounts/Radionuclides** - right side.

3.5.1. Intake Regimes and Units

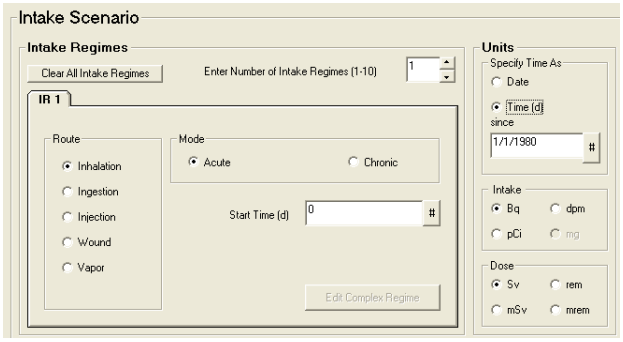


Figure 3.29. Intake Regimes sub-panel with adjacent **Units** sub-panel.

Figure 3.29 shows the ***Intake Regimes*** sub-panel, together with the adjacent **Units** sub-panel, as they appear when IMBA Expert™ OCAS/ORAU-Edition is run for the first time - or when a "**New**" (blank) parameter file is opened. The functions of these two sub-panels are closely coupled.

3.5.1.1. Intake Regimes Sub-panel

By default, the **Number of Intake Regimes** (Intakes) is set to "**1**". A single **index card** is therefore displayed - with the **Tab** label "**IR 1**." You can *select* up to ***10*** intake regimes (**IRs**). Use the selection arrows on the **Enter Number of Intake Regimes (1-10)** to increase the number of **IRs** - or simply *highlight* and type the required number of **IRs** directly in this box.

For each **IR**, you can ***select***:

- the **Route** of intake (from **Inhalation**, **Ingestion**, Injection, or Wound);
- the **Mode** of intake (from Acute or Chronic);
- the **Start Time (d)** of intake.

With the ***Units*** of **Time** at the default setting of "**Time (d) since**," *Selecting* the ***Chronic*** **Mode** automatically displays an additional dialog box - the **End Time (d)** box - for you to specify the end of the period of chronic intake (Figure 3.30).

In both the **Start Time (d)** and **End Time (d)** boxes, you enter the time value in **integer** or **decimal-fraction** days, relative to the *reference* "**Time (d) since**" value**.** For example, with the "**Time (d) since**" time-of-day set at 7:00:00 AM.

- 0, 5 - *start time* is the zeroth day (at 7:00 AM), *end time* is the fifth day (at 7:00 AM);
- 0.4375, 6.75 - *start time* is the zeroth day (at 5:30 PM), *end time* is the sixth day (at 1:00 AM).

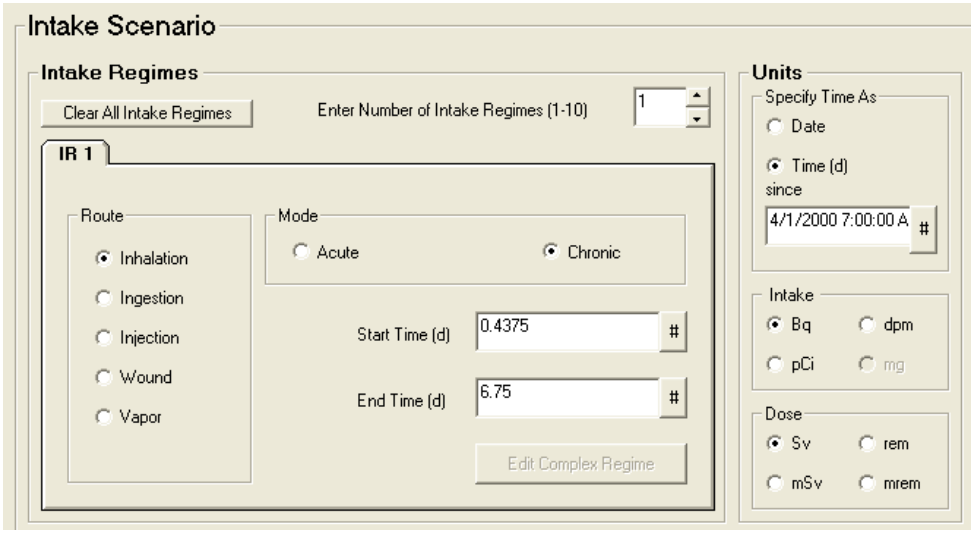


Figure 3.30. The **End Time (d)** dialog box appears when you select the ***Chronic*** intake **Mode** - for the displayed **IR** only.

Note: IMBA Expert™ OCAS/ORAU-Edition automatically detects the "Country Setting" of your computer - and automatically displays all dates in your correct "Date Convention." However, to ensure global "transportability" of data files, the Parameter.ix file stores all dates in the U.S. date convention, *i.e.*, as MM/DD/YYYY.

Tip: Take care when using two-digits to specify the year (YY). By convention, "00 - 29" is automatically interpreted by Windows as "2000 - 2029" - and "30 - 99" as "1930 - 1999." If in any doubt, it is safest to use four-digits to specify the year (YYYY). If you want to specify 2030, then you MUST enter "2030!"

3.5.1.2. Reference Date (and Time)

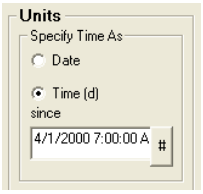


Figure 3.31. The *reference* "**Time (d) since**" value.

For all calculations of bioassay quantities (as a function of time), and to plot graphs, IMBA Expert™ OCAS/ORAU-Edition uses a single, common timescale. The starting point of this timescale is defined by the **Date (and Time-of-Day)** entered in the "**Time (d) since**" dialog box. The "pre-loaded" default starting value is 1/1/1980 (January 1st, 1980) - see Figure 3.29.

Note: For every **IR**, IMBA Expert™ OCAS/ORAU-Edition automatically tracks **Time** values relative to the single **Reference Date (and Time)** that is displayed in the **Units** sub-panel - in the "**Time (d) since**" dialog box.

Key Tip: As the first step in entering your data in IMBA Expert™ OCAS/ORAU-Edition, *change* the default value in the "**Time (d) since**" dialog box to a Date/Time-of-Day that is appropriate for your data. For example: (1) the starting date and time of the first intake that you want to analyze, or (2) the start of employment - for a complex case involving multiple intakes over an extended period of years.

3.5.1.3. Units Sub-panel to Specify Time

This is used to switch the ***Unit*** in which **Time** is displayed. Under the heading "**Specify Time As**," you can *select*:

- **Date** - to display **Start** and **End** times as **Date + hh:mm:ss**, or;
- **Time (d) since** - the default setting, to display **Start** and **End** times as **decimal-fraction days**.

Figure 3.32 shows how the Figure 3.30 display changes when you switch to the **Date** *option*.

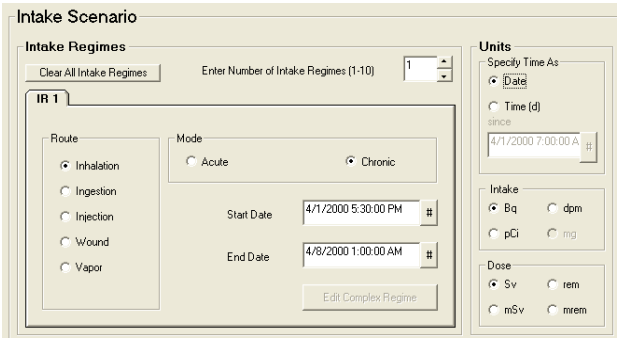


Figure 3.32. The **Start Date (and time-of-day)** and **End Date (and time-of-day)** appear automatically (in the ***Chronic*** intake **Mode**) when you select **Date** under "**Specify Time As**."

Note: In the example shown in Figures 3.30 and 3.31, the **Reference Date (and Time)** is 04/01/00 07:00 AM (April 1st, 2000 at 07:00 - **in U.S. Date convention**). The **Start Time (d)** for **IR1** is "**0.4375**" - so the **Start Date** of the ***Chronic*** intake is set automatically as **April 1st, 2000 at 5:30:00 PM** (by adding "**0.4375 d**" to the **reference date and time**). Similarly, the **End Date** is set automatically by adding "**6.75 d**" to the **Reference Date (and Time)**.

Note: the selected "**Specify Time As**" setting will be applied automatically throughout IMBA Expert™ OCAS/ORAU-Edition - in all three screens (**Main Screen**, **Bioassay Calculations** and **Dose Calculations**).

Tip: at any time during your use of IMBA Expert™ OCAS/ORAU-Edition (except when a calculation is underway), you can return to the **Main Screen** (and the ***Units*** sub-panel) - to switch the **Unit** for ALL displayed **Time** values. This has NO effect on the calculated results. It simply enables you to match the **Time** display to the time-unit convention used in your data files - or to your own preference for direct data entry.

3.5.1.4. Drop-down Calendars

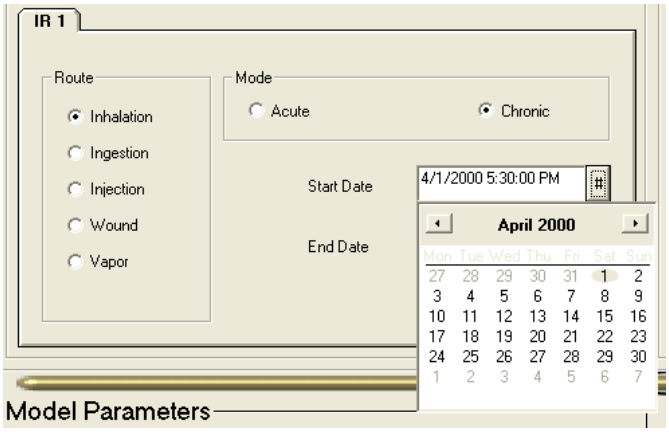


Figure 3.33. Drop-down Windows® **Calendar** for date selection.

As an alternative to *typing* in the full **Date** directly in the dialog box, *clicking* the "#" sign to the right of each of IMBA Expert™ OCAS/ORAU-Edition's **Date** dialog boxes brings up the Windows **Calendar** tool. Use your mouse pointer to select the required **day** in the displayed month - if necessary, use the Calendar's *arrow buttons* to ***scroll*** backwards or forwards through the months (and years). *Click* on the required **Date** to load this into the associated dialog box (*e.g.*, as **MM:DD:YYYY for U.S. date settings**). The Calendar will close automatically.

Once you have registered the correct **Date** in the dialog box, you can move your mouse pointer to the **right** of the displayed **Date**, *click*, *type* a "**space**," and then *type* in any specific "**time-of-day**." If you don't add the time-of-day, IMBA Expert™ OCAS/ORAU-Edition interprets this as 00:00 AM (midnight).

Tip: If the **Calendar** is not already set on your desired **Year** when first opened, it is usually quicker to overtype the **YYYY** value shown in the associated dialog box - before using the **Calendar** to find the required day or month.

Tip: To close the **Calendar** without changing the previously displayed **Date** in the dialog box, *re-click* the "#" sign next to the dialog box.

3.5.2. Specifying Several Intake Regimes

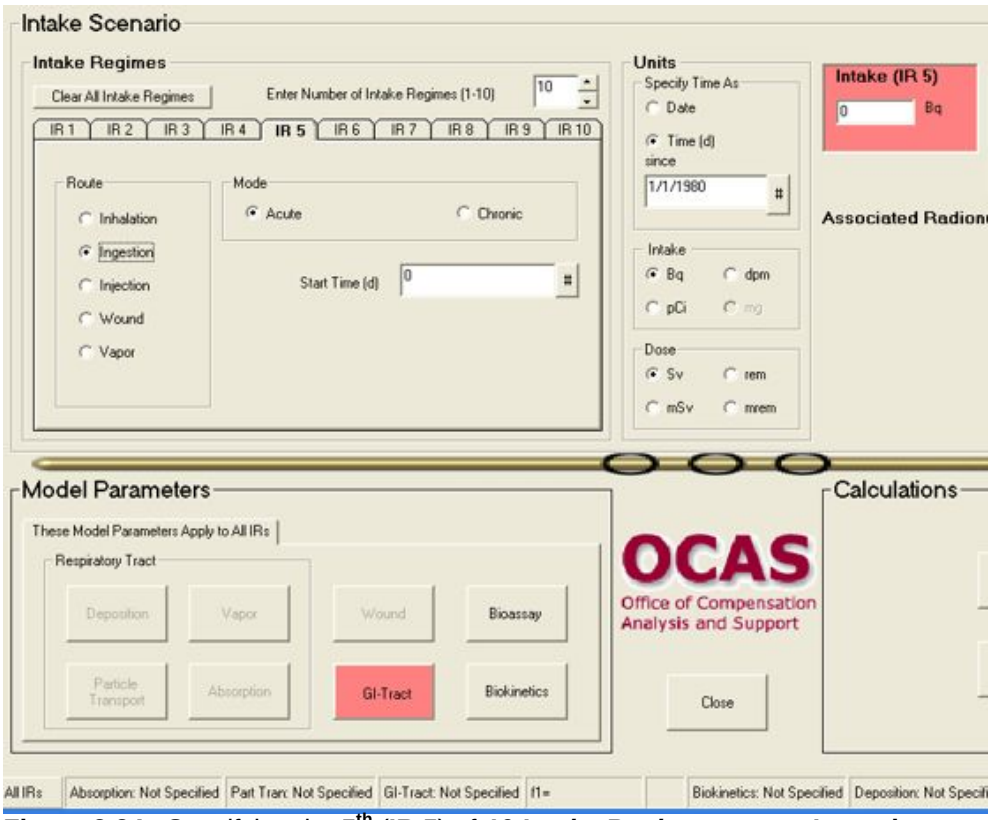


Figure 3.34. Specifying the **5th** (**IR 5**) of ***10 Intake Regimes*** - as an **Ingestion**.

Figure 3.34 shows how to set up IMBA Expert™ OCAS/ORAU-Edition to assess **multiple intakes** - a total of **10** intakes in this case. The ***Intake Regimes*** sub-panel displays one intake at-a-time. The fifth intake (**IR 5**) is shown here. This is an **Ingestion**. In this case, IMBA Expert™ OCAS/ORAU-Edition is set up to define independently the model parameters for **IR 5**, as indicated in the ***Status Bar*** (bottom row left).

The set-up steps are:

1. **Enter Number of Intake Regimes (1-10)** - *select* **10**.
2. *Select* the ***Advanced*** menu (from the ***Main Screen*** menu bar).
3. *De-select* (*un-check*) the default "**Apply Model Params to All IRs**" *option* - this enables the **model parameters** to be set up **independently** for all **IRs**.
4. *Select* the index **Tab** for **IR 5**.
5. *Select* "**Ingestion**" as the ***Route*** of intake.
6. *Select* the appropriate ***Units*** under "**Specify Time As**" - in this case "**Date**."
7. *Select* the ***Start Date*** of the intake.

In **Step 4**, as the index **Tab** for **IR 5** is selected, the label of the **Intake** dialog box (top-right-corner of Figure 3.34) changes automatically to "***Intake (IR 5)***." This enables you to specify a (hypothetical) **intake amount** for the selected **intake regime** (**IR 5**).

In **Step 5**, as soon as "**Ingestion**" is selected, the ***Model Parameters*** display for **IR 5** changes - to highlight the "**Ingestion**" button in red. This flags that it is necessary for you to define the **Ingestion** model parameters (as described under Model Parameters Sub-panel). Whichever

"***Route*** of intake" *option* you *select*, IMBA Expert™ OCAS/ORAU-Edition will *red-flag* in the ***Model Parameters*** sub-panel the associated **models** (parameters) that still need to be **defined** before any calculations can be performed.

3.5.3. Activity Units of Intake

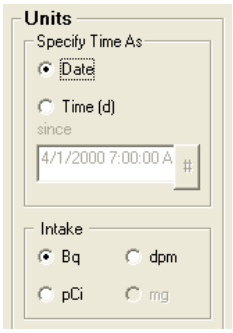


Figure 3.35. Specifying the activity ***Units*** of ***Intake***.

You can *select* to work in:

- the **International** (SI) unit of activity - **Bq** (bequerel);
- the **Traditional** units of activity - **dpm** (disintegrations per minute), **pCi** (pico-curie).

	Important Note: The "**mg**" unit is also available when you select the indicator nuclide as "**Uranium Mixtures**". The "**mg**" unit is used to specify measurements of **mass**, *e.g.*, measurements of the mass of uranium in urine, by phosphorescence or mass spectrometry.
	Warning: The selected working **Unit** of activity is used throughout IMBA Expert™ OCAS/ORAU-Edition. You will need to **ensure** that this activity **Unit** is **consistent** with the activity unit in which your **bioassay data** are expressed. Although the working activity **Unit** will NOT affect the calculated **value(s)** of **intake(s)**, it WILL affect crucially the **calculated doses**.

3.5.4. Units of Dose

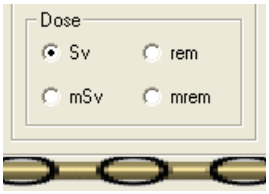


Figure 3.36. Specifying the ***Units*** of ***Dose***.

From the ***Units*** sub-panel, you can ***select*** the ***Unit*** of ***Dose*** to be:

- **International (SI)** - either **Sv** (sievert) or **mSv**;
- **Traditional** - either **rem** or **mrem**.

	Warning: You can change the **Unit** in which doses are displayed at will - but you MUST re-run your dose calculation to change the displayed **values** of dose accordingly.

Note: All doses (equivalent or effective) calculated by IMBA Expert™ OCAS/ORAU-Edition are 50-y committed doses.

3.6. Intake Amounts/Radionuclides Sub-panel

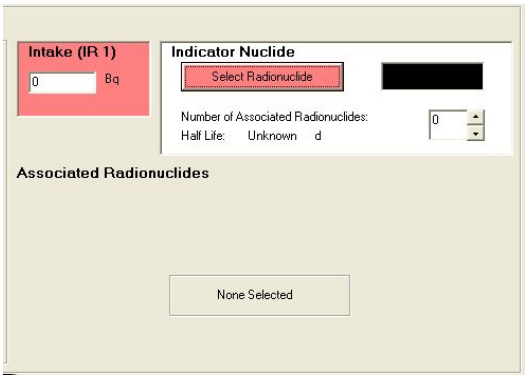


Figure 3.37. Specifying the **Indicator Nuclide** and **Intake** amount.

Figure 3.37 shows the sub-panel for specifying **intake amounts** and **radionuclides**, as it appears when **IMBA Expert™ OCAS-Edition** is run for the first time - or when a "**New**" (blank) parameter file is opened. Notice that the small panel labeled **"Intake (IR 1)" is** *highlighted* in red - as is the "**Select Radionuclide**" button. This warns that neither an **intake amount** nor an **Indicator Nuclide** has been defined.

Note: IMBA Expert™ OCAS/ORAU-Edition works with a SINGLE **Indicator Nuclide** for each case study, *i.e.*, the **parameter file** holds only ONE **indicator nuclide**. If you need to assess bioassay measurements of more than one **indicator nuclide** for an individual person, you will need to set up a separate case study (**parameter file**) for each **indicator nuclide**.

Note: The **Intake (IR #)** amount applies only to the **Indicator Nuclide**. The activity of **Associated Radionuclides** is defined separately - as an activity **Abundance (%)** relative to the activity of the indicator nuclide.

3.6.1. Selecting the Indicator Nuclide

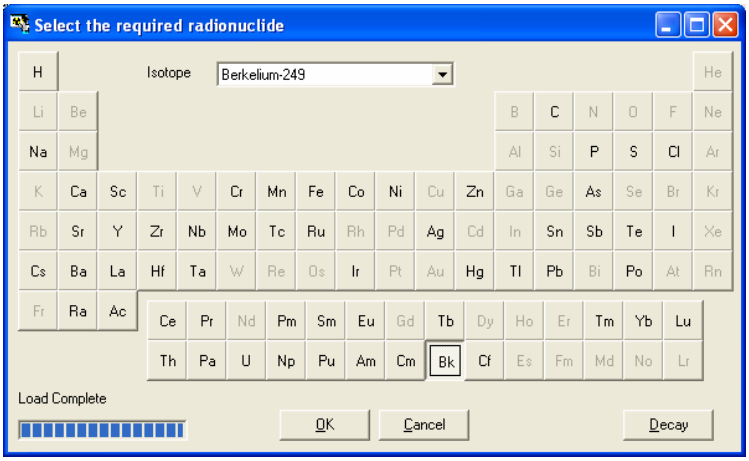


Figure 3.38. Selecting the ***Indicator Nuclide*** from the periodic table of the elements.

The ***Indicator Nuclide*** is selected from the periodic table of the elements (Figure 3.38). To display this, *click* the "**Select Radionuclide**" *button* (top right-corner of **Main Screen**). To *select* a specific **radionuclide**:

1. *Click* the required **element** - this puts the first **isotope** available for that element in the ***Isotope*** dialog box.
2. *Click* the "**down**" arrow on the ***Isotope*** dialog box - this displays all the available isotopes for that element.
3. *Highlight* and *click* your required **isotope** from the drop-down list - this puts your isotope in the dialog box (Figure 3.39).
4. *Click* the "***OK***" *button* in the "**Select the required radionuclide**" window to **confirm** your choice - and **load** your chosen radionuclide as the ***Indicator Nuclide***.

Note: When you open the "**Select the required radionuclide**", you will see the (blue) progress bar move in the lower-left corner of the window. This indicates "**Load Complete**", *i.e.*, that your IMBA Expert™ OCAS/ORAU-Edition software has "**loaded**" all of your available radionuclides.

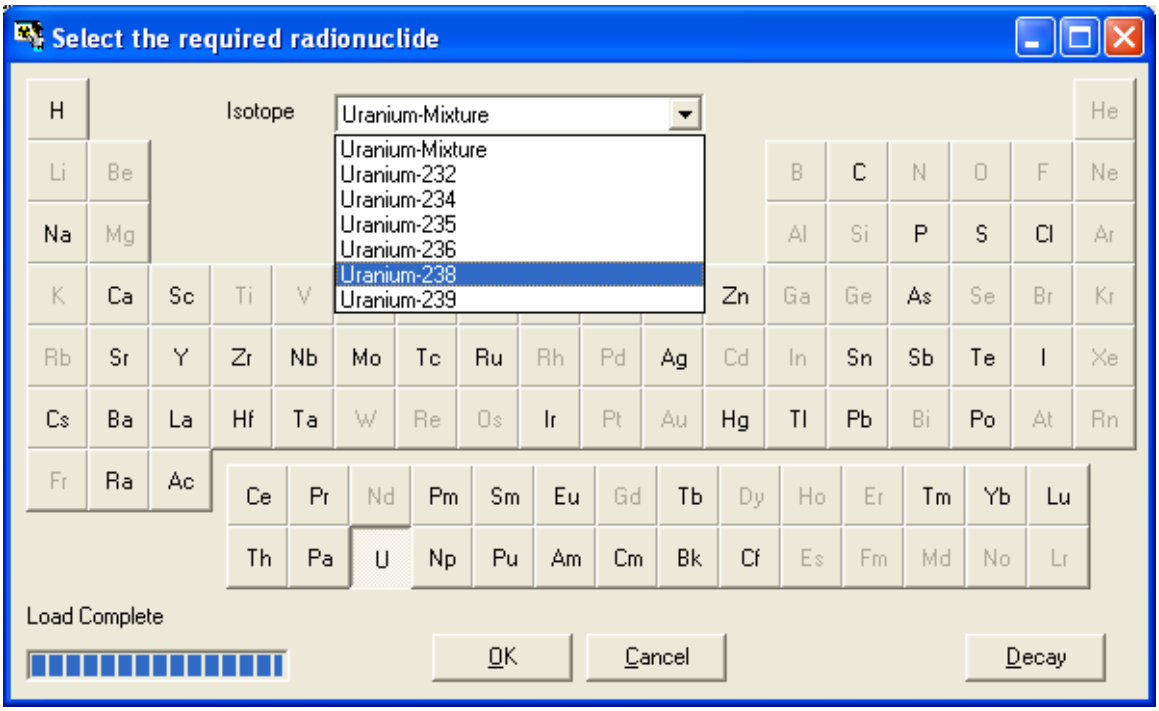


Figure 3.39. Selecting **Uranium-238** from the ***Isotope*** drop-down list.

Clicking "OK" closes the "**Select the required radionuclide**" window - and displays the radionuclide in the ***Indicator Nuclide*** window (top-right-corner of the **Main Screen**), as shown in Figure 3.40. Once a radionuclide has been selected the red *highlight* on the "**Select Radionuclide**" *button* disappears.

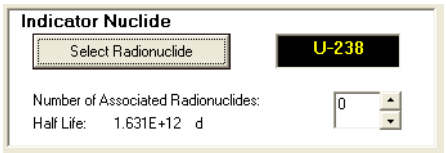


Figure 3.40. The **selected radionuclide** displayed in the ***Indicator Nuclide*** window.

3.6.1.1. List of Available Radionuclides

The radionuclides implemented in IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) are:

- **actinium** (^{227,228}Ac);
- **americium** (^{241,243}Am);
- **antimony** (^{124,125}Sb);
- **arsenic** (^{74}As);
- **barium** (^{133,140}Ba);
- **berkelium** (^{249}Bk);
- **calcium** (^{45}Ca);
- **californium** (^{2249,252}Cf);
- **carbon** (^{14}C);
- **cerium** (^{139,141,143,144}Ce);
- **cesium** (^{134,137}Cs);
- **chlorine** (^{36}Cl);
- **chromium** (^{51}Cr);
- **cobalt** (^{57,58,60}Co);
- **curium** (^{242,243,244}Cm);
- **europium** (^{152,154,155,156}Eu);
- **hafnium** (^{181}Hf);
- **hydrogen [tritium]** (^{3}H);
- **iodine** (^{125,129,131,133,134,135}I);
- **iridium** (^{192}Ir);
- **iron** (^{55,59}Fe);
- **lanthanum** (^{140}La);
- **lead** (^{210}Pb);
- **lutetium** (^{174}Lu);
- **manganese** (^{54}Mn);
- **mercury** (^{203}Hg);
- **molybdenum** (^{99}Mo);
- **neptunium** (^{237,239}Np);
- **nickel** (^{63}Ni);
- **niobium** (^{94,95}Nb);
- **phosphorus** (^{32,33}P);
- **plutonium** (^{238,239,240,241,242}Pu);
- **polonium** (^{208,209,210}Po);
- **praseodymium** (^{143,147}Pr);
- **promethium** (^{147}Pm);
- **protactinium** (^{231,233,234}Pa);
- **radium** (^{223,224,226,228}Ra);
- **ruthenium** (^{103,106}Ru);
- **samarium** (^{151}Sm);
- **scandium** (^{46}Sc);
- **silver** (^{110m}Ag);
- **sodium** (^{22,24}Na);
- **strontium** (^{85,89,90,91}Sr);

- **sulfur** (^{35}S);
- **tantalum** (^{182}Ta);
- **technetium** (^{99}Tc);
- **tellurium** (^{131,131m}Te);
- **terbium** (^{160}Tb);
- **thallium** (^{201,202,204}Th);
- **thorium** (^{228,230,232,234}Th);
- **thulium** (^{170}Tm);
- **tin** (^{113}Sn);
- **uranium** (^{232,234,235,236,238,239}U and U-Mixtures);
- **ytterbium** (^{169}Yb);
- **yttrium** (^{88,90,91}Y);
- **zinc** (^{65}Zn);
- **zirconium** (^{95}Zr).

3.6.1.2. Displaying the Decay Series

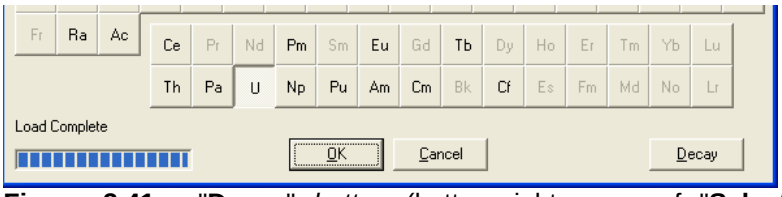


Figure 3.41. "**Decay**" *button* (bottom-right-corner of "**Select the required radionuclide**" window).

To display the complete decay chain of your selected radionuclide, you *click* the "**Decay**" *button* in the "**Select the required radionuclide**" window (Figure 3.41). The "**Decay chain of **-*****" window will open (where "****-*****") is the selected radionuclide. Figure 3.42 shows the "**Decay chain of U-238**" window as it first appears (partial view).

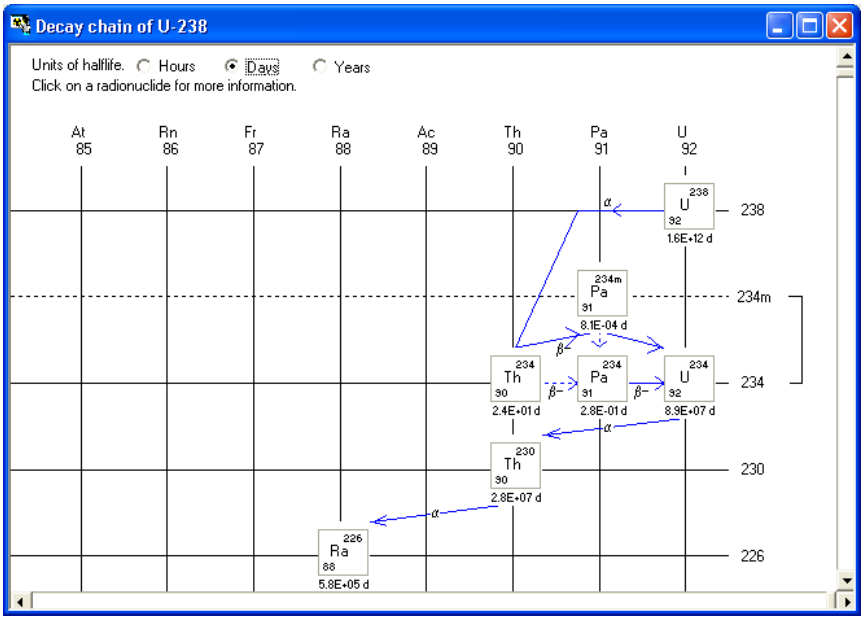


Figure 3.42. "**Decay chain of U-238**" window - partial view.

For a long decay chain (such as that of ^{238}U), you can view the whole chain by hitting the Windows® "maximize" *button* (center of the three-button cluster, top-right-corner of Figure 3.42). The complete decay chain will then be "re-sized" to fit your whole screen (Figure 3.43).

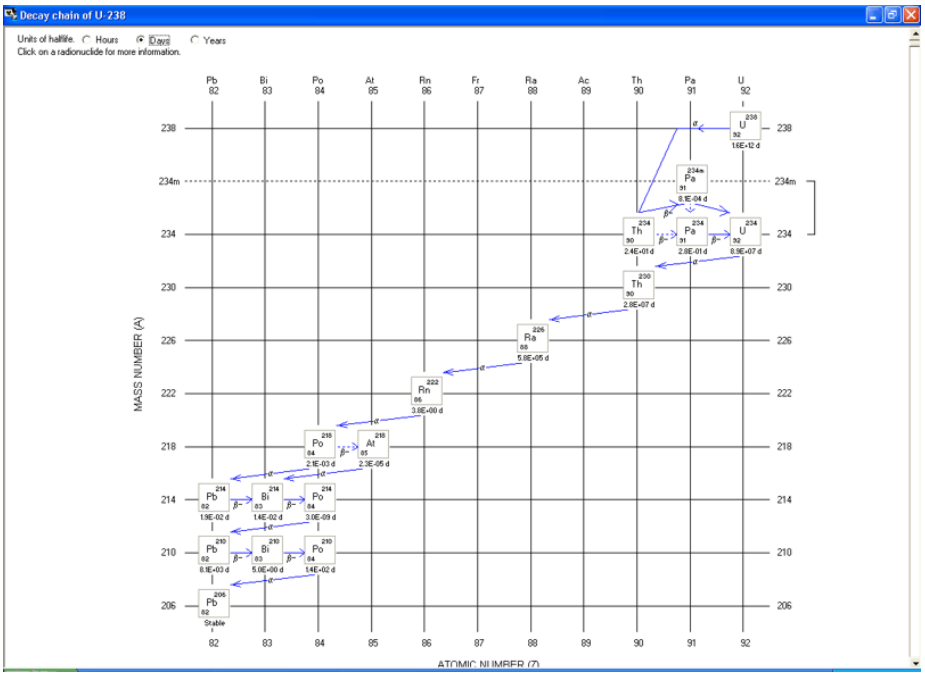

Decay chain of U-238
Units of halflife. Hours Days Years
Click on a radionuclide for more information.
MASS NUMBER (A)
ATOMIC NUMBER (Z)

Figure 3.43. Maximized view of the whole "**Decay chain of U-238**" window.

To exit this window, *click* the Windows® "**Exit**" *button* ("**X**" - in the top-right-corner). This will return you to the **Main Screen** - leaving the "**Select the required radionuclide**" still open. *Click* this window's own "**X**" button to close it.

3.6.1.3. Displaying the ICRP38 Radiation Data

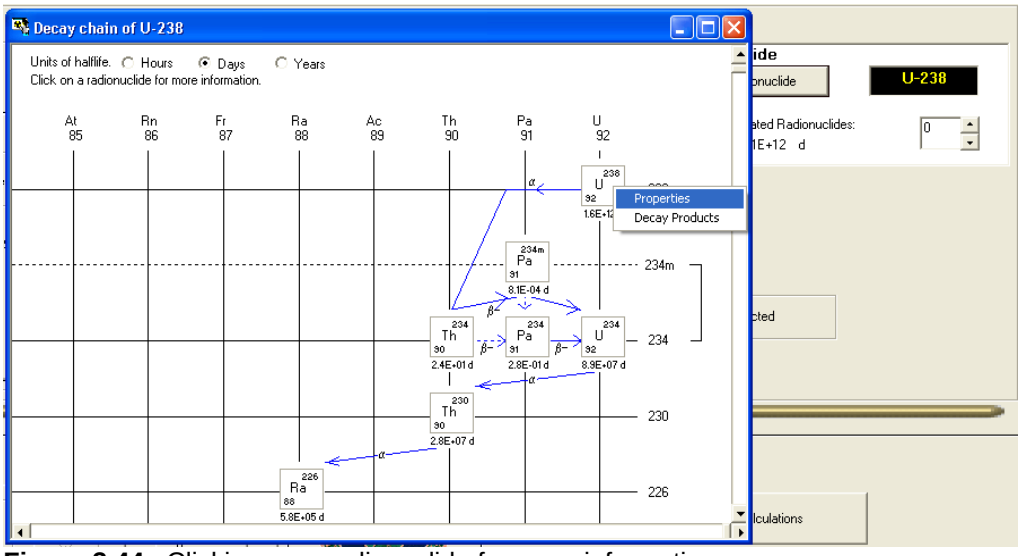


Figure 3.44. Clicking on a radionuclide for more information.

In the "**Decay Chain**" window, you can display the ICRP Publication 38 radiation data for each radionuclide - by *clicking* on the radionuclide (Figure 3.44). *Highlight* either the "**Properties**" or "**Particle Energies**" *option* and *click* to display the respective radiation data.

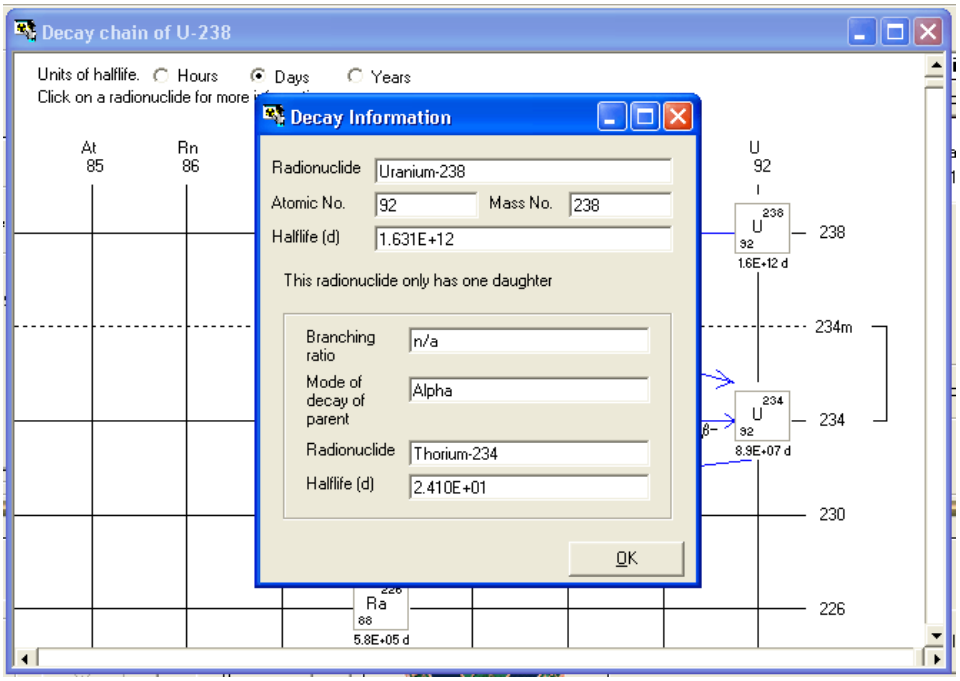


Figure 3.45. Displaying the **Decay Information** for Uranium-238.

Figure 3.45 shows the "**Decay Information**" window that appears when you *click* the "**Properties**" *option* for ^{238}**U**. You can pre-select the displayed "**Units of halflife**" (hours, days, or years) in the "**Decay chain**" window. Figure 3.46 shows the "**Energies of decay products**" window that appears when you *click* the "**Particle Energies**" *option* in the "**Decay chain of U-238**" window (Figure 3.44).

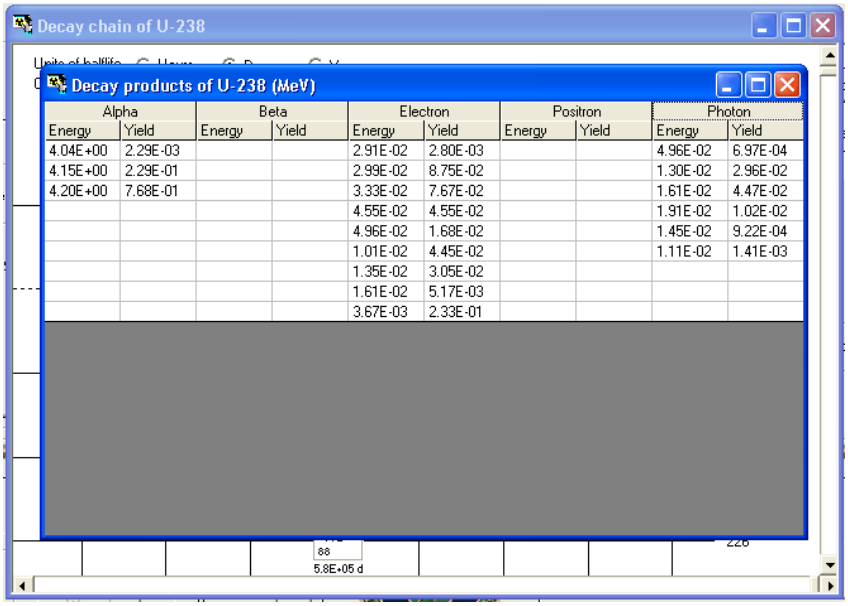


Figure 3.46. Displaying the **Energies of decay products** for Uranium-238.

3.6.2. Selecting Associated Radionuclides

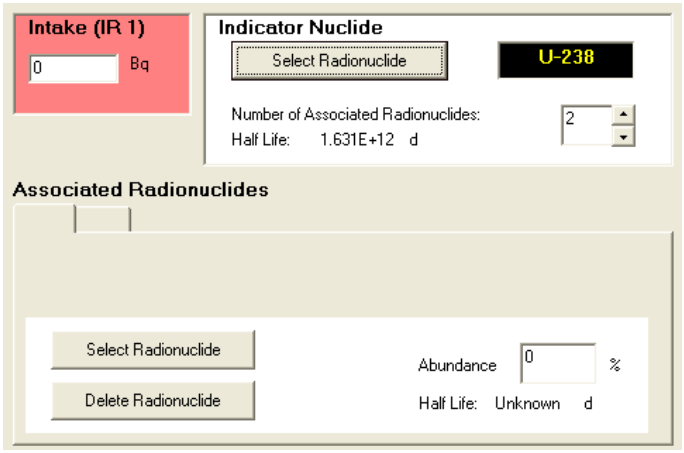


Figure 3.47. Adding **Associated Radionuclides** to the **Indicator Nuclide**.

To add one or several **Associated Radionuclides**, you first *select* the number of radionuclides required. This automatically displays the required number of blank "record cards" (Figure 3.47). You can then use the "**Select Radionuclide**" *button* to *select* each associated radionuclide from the periodic table of elements - as you did for the **Indicator Nuclide**. You also need to ***define*** the "**Abundance**" (%) for each associated radionuclide - relative to the activity of the **Indicator Nuclide** in the **Intake**. Figure 3.48 shows **two** additional radionuclides (^{239}**Pu** and ^{241}**Am**) set up to be associated with a hypothetical (**1 Bq**) **Intake** of the indicator nuclide (^{238}**U**). The "**Delete Radionuclide**" *button* removes the indexed associated radionuclide.

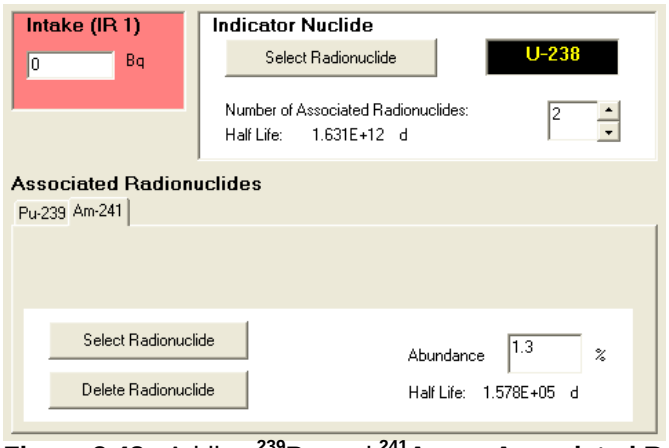


Figure 3.48. Adding ^{239}**Pu** and ^{241}**Am** as **Associated Radionuclides**.

	Note: The **Associated Radionuclides** are not part of any **bioassay calculation**. All bioassay calculations are performed for the **Indicator Nuclide**. The associated radionuclides represent additional **Intakes** - that ARE included in any **dose calculation**.
	Warning: If there is more than one **Intake Regime** (**IR**), then IMBA Expert™ OCAS/ORAU-Edition automatically assigns the same **Associated Radionuclides** (and their specified **Abundances**) to **All IRs**. If this is **not appropriate**, you should *calculate* doses separately for each **IR** - using its own set of **Associated Radionuclides** and/or **Abundances**.

3.6.3. Using Uranium Isotopic Mixtures

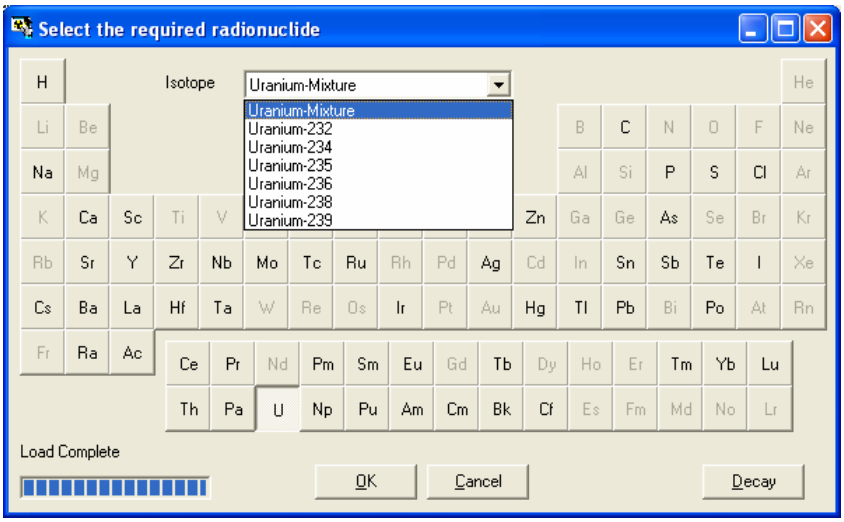


Figure 3.49. Selecting **Uranium-Mixture**.

IMBA Expert™ OCAS/ORAU-Edition enables you to specify *intake(s)* consisting of a *mixture of uranium isotopes*. To do this, *select* "**Uranium-Mixture**" from the drop-down list of uranium isotopes (Figure 3.49). *Clicking* "**OK**" then returns you to the **Main Screen** - and a new "**Specify U Mixture**" button will appear automatically under the "**Intake (IR1)**" box (Figure 3.50).

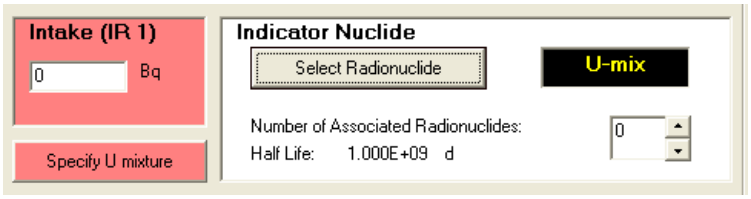


Figure 3.50. The "**Specify U Mixture**" button.

Clicking the "**Specify U Mixture**" button *opens* the "**Details of uranium mixture**" window (Figure 3.51).

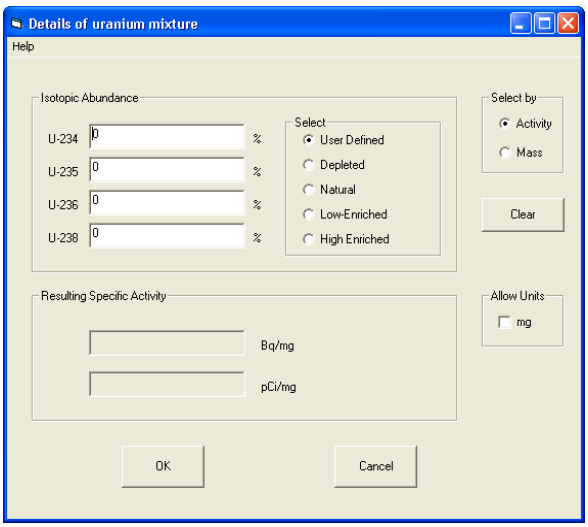


Figure 3.51. The "**Details of uranium mixture**" window with the default **User Defined** option and default "**Select by**" **Activity**.

Entry of any non-zero value for an Isotopic Abundance causes IMBA Expert™ OCAS/ORAU-Edition to *calculate* and *display* automatically the Resulting Specific Activity of the uranium. This is displayed in both international and traditional units of activity, Bq and pCi, respectively, in the composite units **Bq/mg** and **pCi/mg** (Figure 3.52).

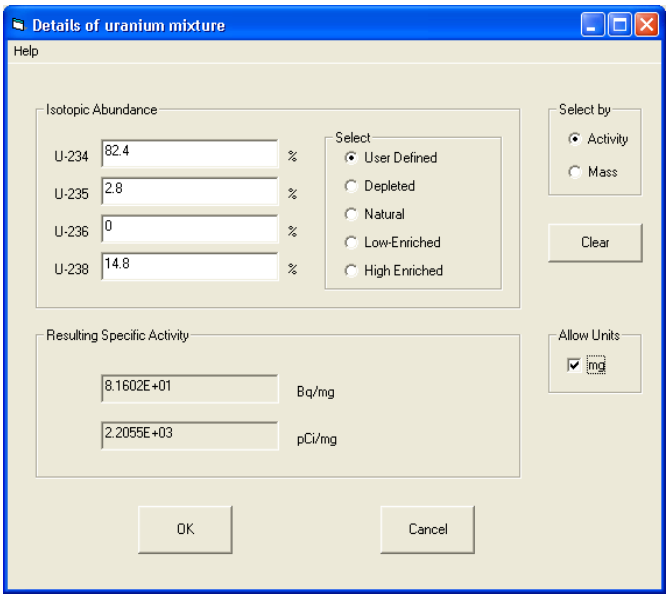


Figure 3.52. Selection of **User Defined** values of the uranium isotopic composition by **Activity**.

Checking the "**Allow Units**" **mg** box enables bioassay quantities (and intakes) to be specified in **mass units** (**mg**). This is useful for *uranium urinalysis*, where the mass of uranium is measured in urine samples, rather than its activity.

Clicking the "**OK**" button (Figure 3.52) loads the displayed values of isotopic composition and specific activity into the **Parameter file**, *closes* the "**Details of uranium mixture**" window, and *returns* you to the **Main Screen**. IMBA Expert™ OCAS/ORAU-Edition (Phase II) then implements your selected "**U Mixture**" - by setting up automatically the four isotopic components as Associated Radionuclides (Figure 3.53). The Abundance of each uranium isotope is displayed when you *select* (in turn) its **Index Tab** - starting with "**U-234**" (Figure 3.53).

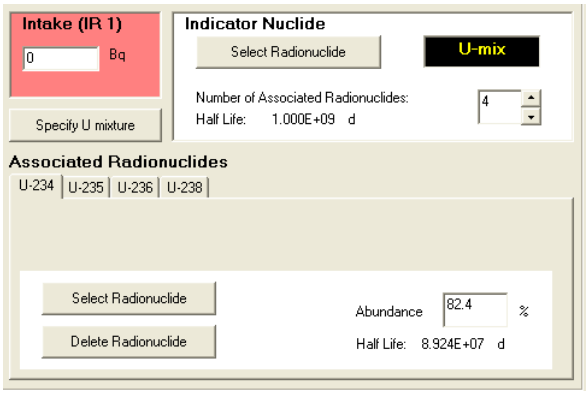


Figure 3.53. Appearance of **Radionuclide/Intake** panel for **User Defined** isotopic mixture shown in Figure 3.52.

	Important: The defined isotopic mixture of **Associated Radionuclides** is assumed for all dose calculations carried out by IMBA Expert™ OCAS-Edition (Phase II). The same mixture is assumed to apply for all intakes.
	Important: BOTH the intake(s) and bioassay quantity are measured in terms of *total uranium* mass *or activity*, as *selected* in the "**Units**" panel), and NOT in terms of the activity or mass of a single isotope. In other words, for bioassay purposes (to calculate intakes), the whole **U Mixture** is treated as the Indicator Nuclide.
	Tip: You can select **default** values of isotopic composition to represent the default types of uranium mixture.

3.6.3.1. Default Types of Uranium Mixture

IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) default sets of Isotopic Abundance values for the main types of uranium mixture. The literature sources of these default values are given in the Technical Basis. **Default** values of **Isotopic Abundance** are given for the following types of uranium:

- Depleted **(DU)**.
- Natural **(U-Nat)**.
- Low-enriched **(LEU)**.
- High-enriched **(HEU)**.

Figures 3.54 - 3.57 show the respective default values, as *selected by Activity*, and the resulting calculated values of Specific Activity. Figure 3.58 shows the corresponding default values of isotopic abundance for **HEU**, as *selected by Mass*.

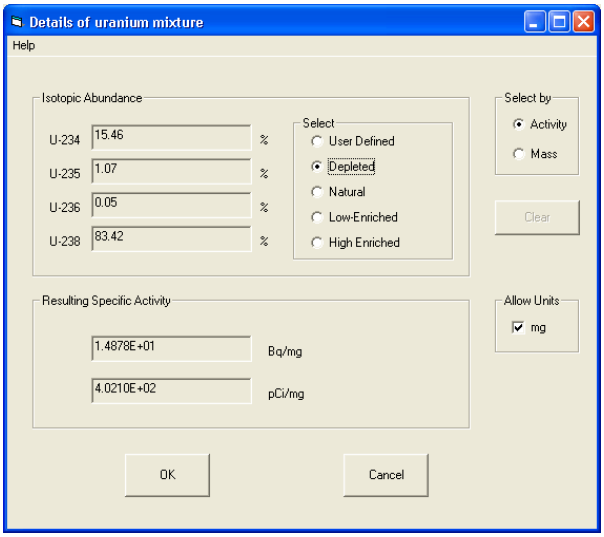


Figure 3.54. Selection of **Depleted** uranium **(DU)** composition by **Activity**.

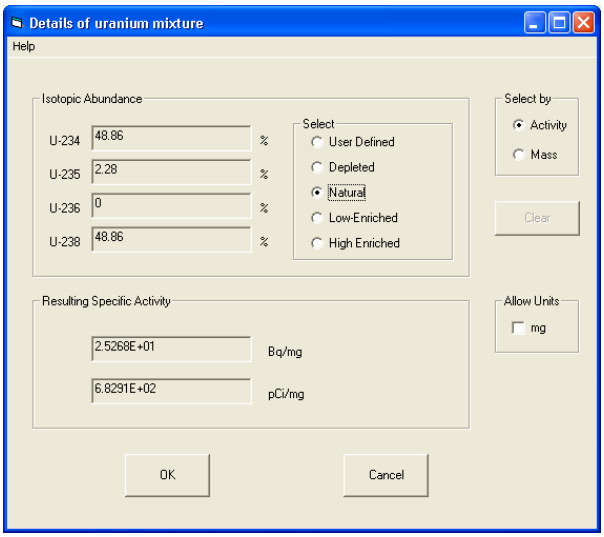


Figure 3.55. Selection of **Natural** uranium **(U-Nat)** composition by **Activity**.

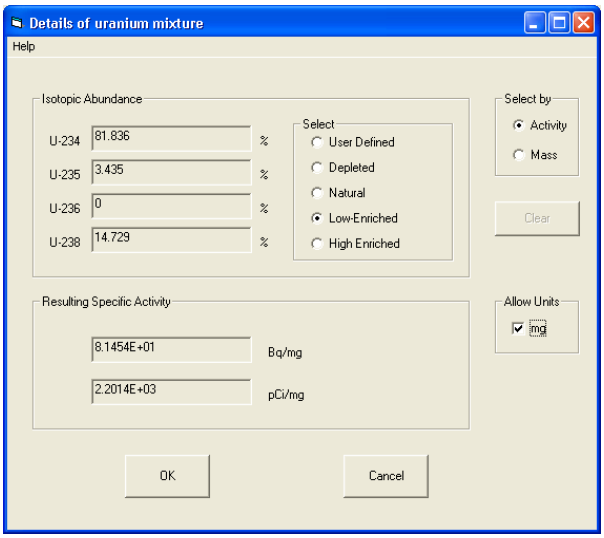


Figure 3.56. Selection of **Low-Enriched** uranium **(LEU)** composition by **Activity**.

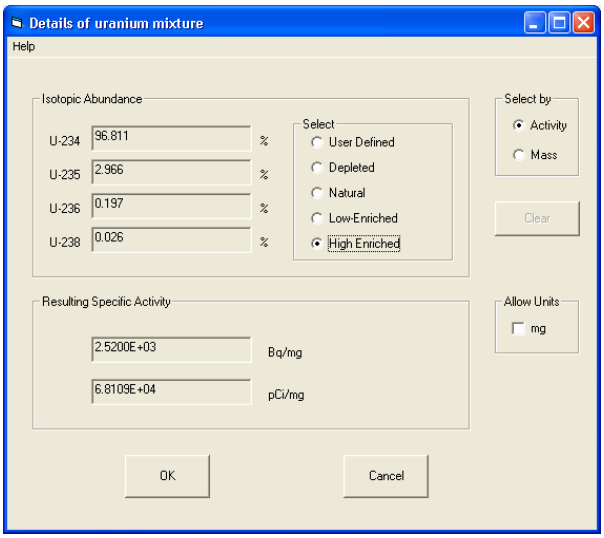


Figure 3.57. Selection of **High-Enriched** uranium **(HEU)** composition by **Activity**.

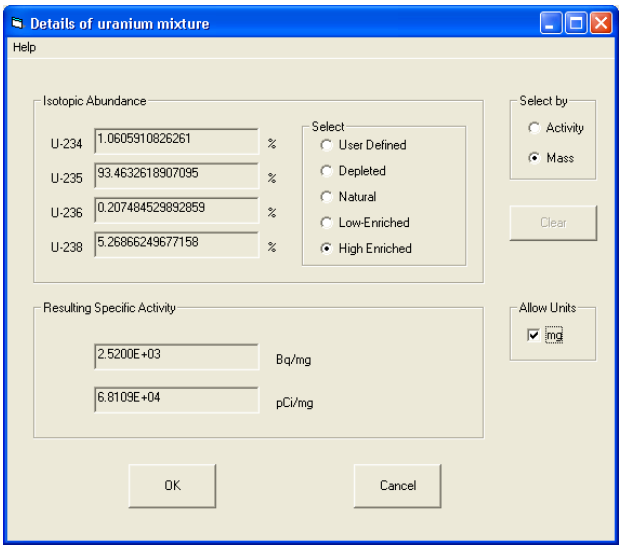


Figure 3.58. Selection of **High-Enriched** uranium **(HEU)** composition by **Mass**.

3.6.4. Setting Hypothetical Intake Amounts

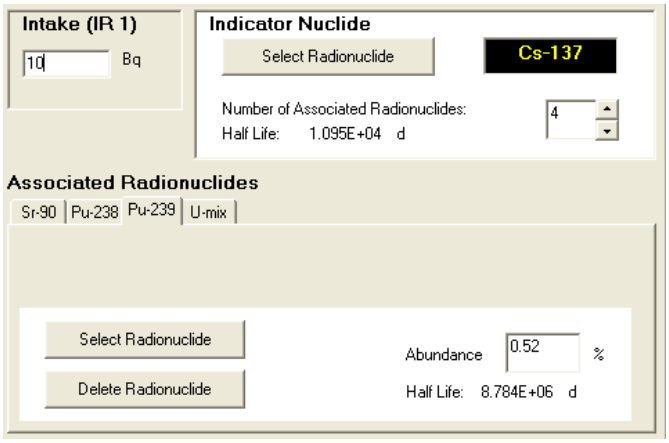


Figure 3.59. Setting a hypothetical amount for **Intake (IR 1)**.

To project **bioassay quantities** and/or **doses** for hypothetical amounts of intake, you can enter an assumed value of intake directly into IMBA Expert™ OCAS/ORAU-Edition - for each **Intake Regime** (**IR**). You do this in the **Intake (IR #)** dialog box (Figure 3.59). If you have more than one **IR**, then *select* each **IR** in turn (from the "**Intake Regimes**" index **Tabs**). Once you have entered a value in the **Intake (IR #)** dialog box, and the program "focus" has left the box, the red *highlight* will be removed automatically for that **Intake (IR #)**. This indicates that the entered intake amount has been stored in memory. However, it will NOT be saved to the **Parameter File** for your case study until "**Save**" is pressed.

	Note: The program "focus" leaves the **Intake (IR #)** dialog box immediately you carry out the next mouse *action*, *e.g.*, when you *click* on another program control.
	Tip: Once you have defined the **IR(s)**, and selected the **Indicator Nuclide**, the **next step** is to proceed with setting up the Model Parameters. You can't perform any calculation in IMBA Expert™ OCAS/ORAU-Edition without first defining the required model parameters. The program will **guide** you through the necessary procedures.

3.7. Model Parameters Sub-panel

3.7.1. Intake by Inhalation

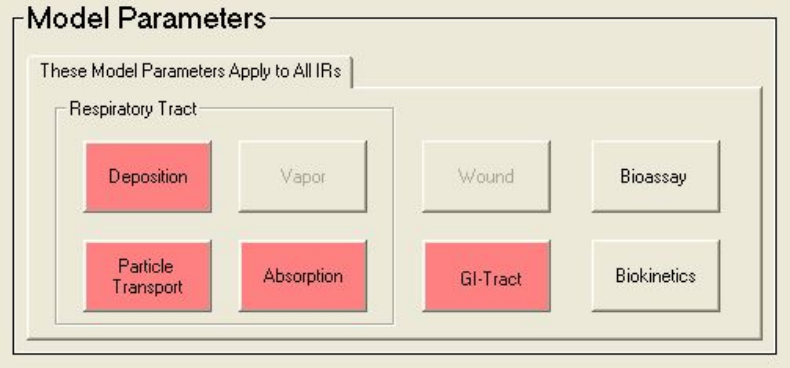


Figure 3.60. Model Parameters sub-panel at start-up - for a **New** (blank) parameter file.

Figure 3.60 shows **Model Parameters** sub-panel as it appears when IMBA Expert™ OCAS/ORAU-Edition is run for the first time, or when a **New** (blank) **parameter file** is loaded. The following "**Model**" *buttons* are *highlighted* in red:

- **Deposition**.
- **Particle Transport**.
- **Absorption**.
- **GI-Tract**.

These *buttons* are *highlighted* because, by default, "**Inhalation**" is selected as the **Route** of intake - and it is necessary for you to *select* the **parameters** for ALL FOUR of these **models** BEFORE you can carry out any calculation. Neither the **Bioassay** nor **Biokinetics** model buttons are *highlighted* at this stage. These WILL be *highlighted* later, when you are preparing to carry out specific **Calculations** (as described later).

Tip: If you attempt to run a calculation without defining the required model parameters, IMBA Expert™ OCAS/ORAU-Edition will display an appropriate WARNING message.

3.7.2. Intake by Ingestion

If you select "**Ingestion**" as the **Route** of intake, the **Model Parameters** sub-panel will change automatically to that shown in Figure 3.61. In this case, the only full **model** required for calculations is the **GI-Tract** model. However, you will also need to specify the **gut uptake fraction** (f_1), which is part of the "**Absorption**" model. In this case, the **absorption parameters** for the **respiratory tract model** are NOT required.

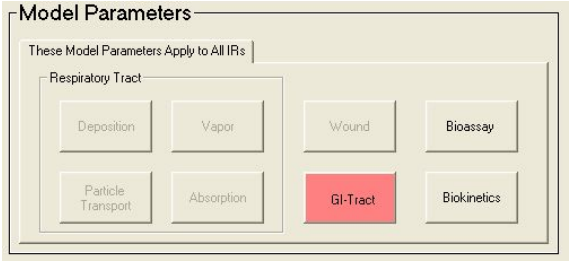


Figure 3.61. Model Parameters sub-panel for "**Ingestion**" as the **Route** of intake.

3.7.3. Intake by Injection

If you *select* "**Injection**" as the **Route** of intake, none of the models *highlighted* above are required, and so none are *highlighted* (Figure 3.62).

Figure 3.62. Model Parameters sub-panel for "**Injection**" as the **Route** of intake.

3.7.4. Intake by Wound

If you select "**Wound**" as the **Route** of intake, the Wound model button is automatically highlighted (Figure 3.63).

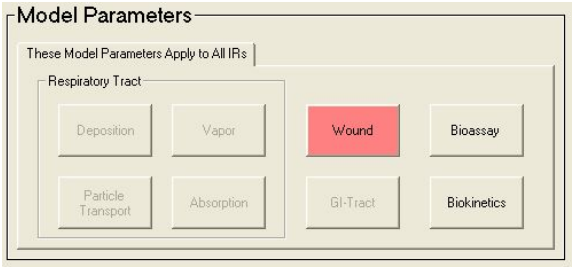


Figure 3.63. Model Parameters sub-panel for "**Wound**" as the **Route** of intake.

3.7.5. Intake of a Vapor

If you select "**Vapor**" as the **Route** of intake, the **Vapor** model button is automatically highlighted - together with the **Particle Transport** and **GI Tract** model buttons (Figure 3.64).

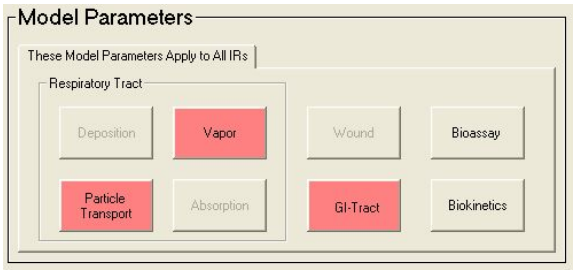


Figure 3.64. Model Parameters sub-panel for "**Vapor**" as the **Route** of intake.

3.8. ICRP-Recommended Model Parameters

3.8.1. Deposition Parameters

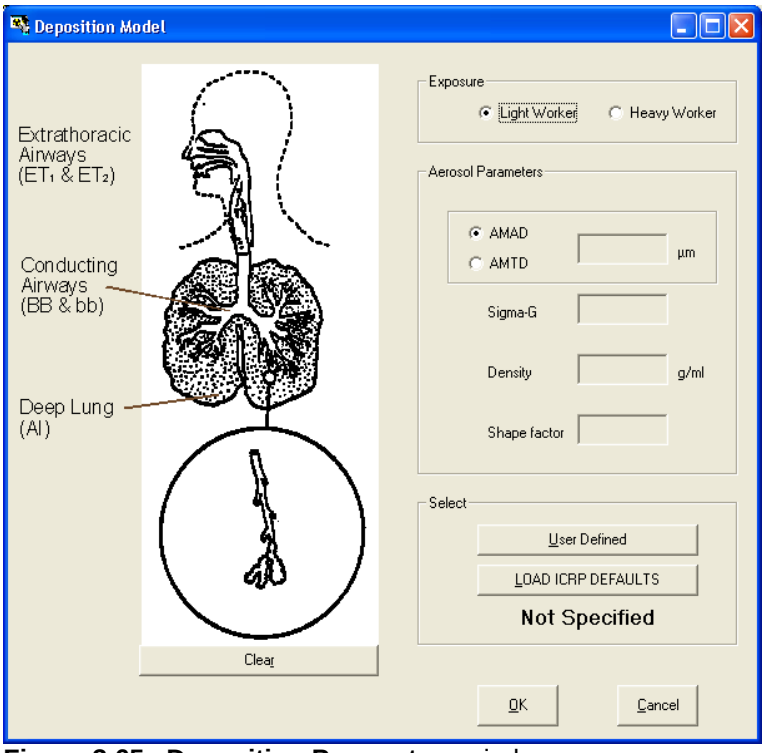


Figure 3.65. Deposition Parameters window.

Clicking the "**Deposition**" *button* in the **Model Parameters** sub-panel (**Respiratory Tract** section) displays the **Deposition Parameters** window (Figure 3.65). This is used to define:

- the exposed worker's Ventilation Rate classification - **Light** work or **Heavy** work;
- the radioactive **Aerosol Parameters**.

IMBA Expert™ OCAS/ORAU-Edition enables you to ***select*** either of two *options* to define the values of the parameters that will be substituted in the *ICRP Publication 66 model* to evaluate the deposition of activity in each region of the respiratory tract for each **Intake Regime** (**IR**):

- **User Defined**;
- **LOAD ICRP DEFAULTS**.

Figure 3.66 shows the parameter values that are used when you **LOAD ICRP DEFAULTS** - by *clicking* the "**LOAD ICRP DEFAULTS**" *button*, followed by the "**OK**" *button*.

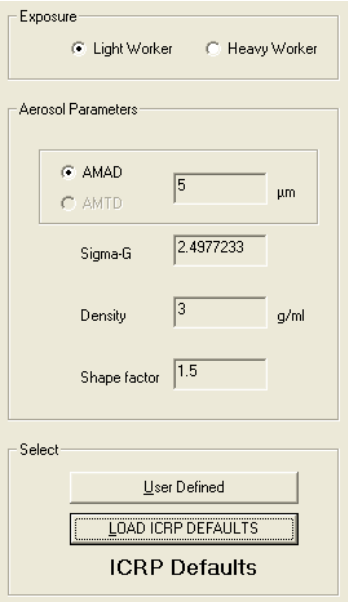


Figure 3.66. Selection of **ICRP Defaults** for **Deposition Parameters**.

The following default parameter values (as recommended in ICRP Publication 66) are loaded:

- Light worker - average ventilation rate 1.2 m^3 h^{-1}.
- AMAD - 5 µm.
- Sigma-G (σ_g) - 2.4977233.
- [Particle] **Density** (ρ) - 3 g cm^{-3}.
- [Particle] Shape Factor (**SF**) - 1.5.

The **Status Bar** automatically indicates the selection of the **ICRP Defaults** for the **Deposition Parameters** (Figure 3.67).

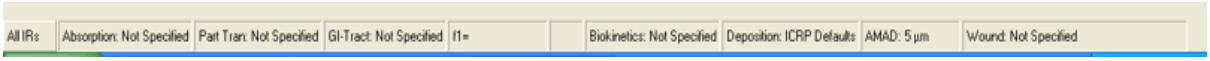


Figure 3.67. Selection of **ICRP Defaults** is automatically indicated on the **Status Bar**.

	Note: As an alternative to the **Light worker**, you can *select* **Heavy worker**. This will evaluate the deposition of activity in each region of the respiratory tract according to the recommendations in *ICRP Publication 66* for representing **heavy work** (average ventilation rate of 1.688 m^3 h^{-1}).
	Warning: If you *select* **Heavy worker** (instead of the ICRP68 Reference Worker classification of the **Light worker**), your "non-standard" selection will NOT be indicated on the **Status Bar**. However, your selection of **Heavy worker** WILL automatically be recorded in the **Parameter File** for your case study.

IMBA Expert™ OCAS/ORAU-Edition also enables you to enter specific values of the **Aerosol Parameters** that may better characterize an intake by inhalation that the default values

recommended in *ICRP Publication 66*. To do this, you *select* the "**User Defined**" option (Figure 3.68).

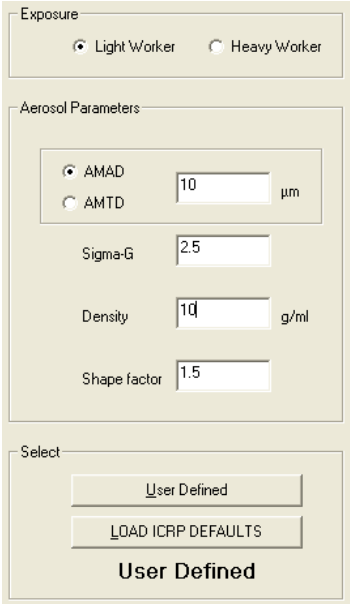


Figure 3.68. Selection of **User Defined** values for **Deposition Parameters**.

In the example shown in Figure 3.68, the following values of **Aerosol Parameters** have been defined:

- AMAD - 10 µm.
- Sigma-G (σ_g) - 2.5.
- [Particle] **Density** (ρ) - 10 g cm^{-3}.
- [Particle] Shape Factor (**SF**) - 1.5.

For these "non-ICRP-default" values, the **Status Bar** automatically indicates the selection of "**User Defined**" **Deposition**, and also shows the selected value of **AMAD** (Figure 3.69).

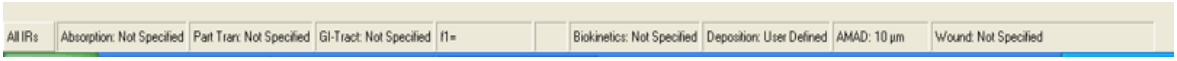


Figure 3.69. Selection of **User Defined** aerosol parameter values is automatically indicated on the **Status Bar**.

To represent sub-micron aerosols, IMBA Expert™ OCAS/ORAU-Edition enables you to define the aerosol AMTD (Figure 3.70). In this case, the **Status Bar** will show the defined value of the **AMTD**.

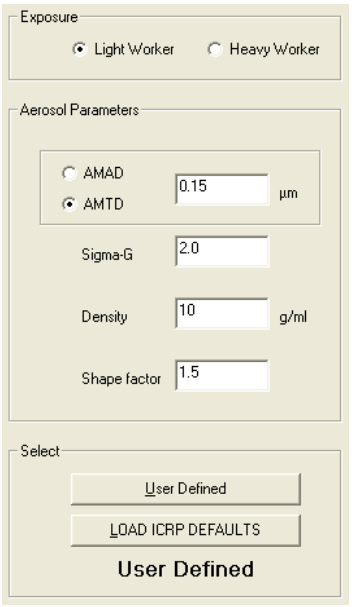


Figure 3.70. Characterizing a sub-micron aerosol by its **AMTD**.

Key Tip: If you are assessing a case with multiple **Intakes** by **Inhalation**, you can define different **Aerosol Parameter** values (and choose either **Light worker** or **Heavy Worker**) independently for EACH **Intake Regime** (**IR**).

3.8.2. Vapor Parameters

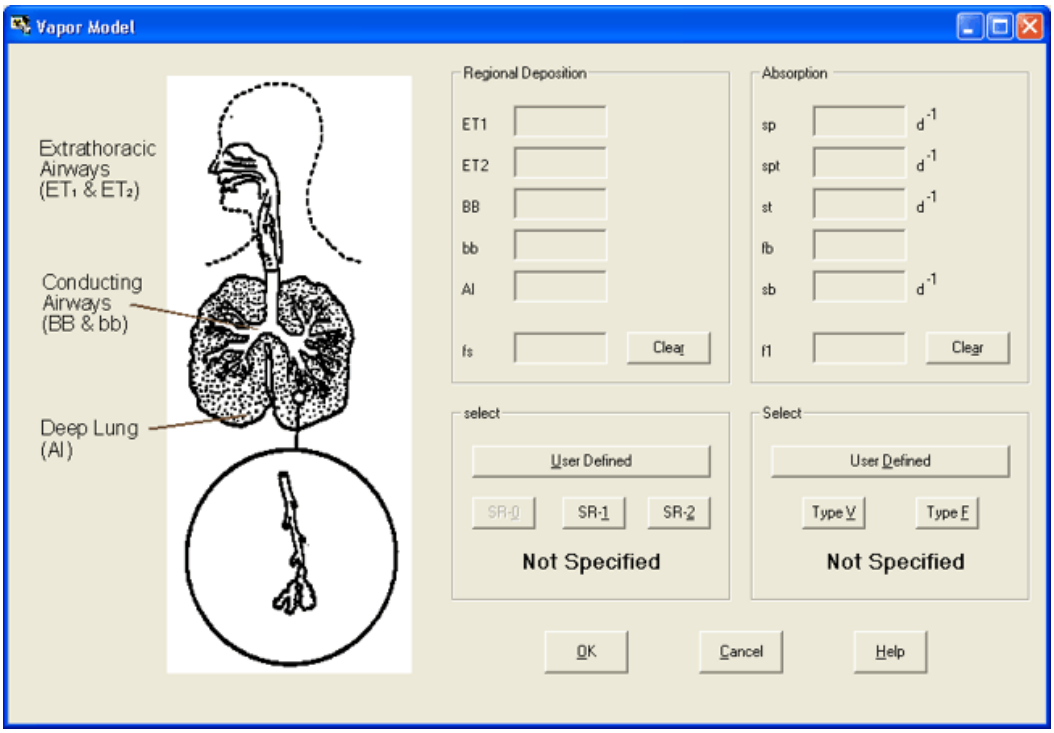


Figure 3.71. Vapor Parameters window.

Clicking the "**Vapor**" *button* in the **Model Parameters** sub-panel (**Respiratory Tract** section) displays the **Vapor Parameters** window (Figure 3.71). This implements the *ICRP Publication 66* model for vapors. The *Vapor Model window* enables you to specify:

- the **type of vapor** (SR-1 or SR-2) which determines its regional deposition in the respiratory tract - or you can define your own (**User Defined**) assumed deposition behavior;
- the subsequent **absorption behavior** (Type V or Type F) - or you can define your own (**User Defined**) assumed absorption behavior.

3.8.2.1. Defining Deposition Behavior

Clicking the "**SR-1**" or "**SR-2**" buttons in the Vapor Model window selects the values of regional deposition shown in Figures 3.72 and 3.73, respectively. *Clicking* "**OK**" then reads these values into IMBA Expert™ OCAS/ORAU-Edition.

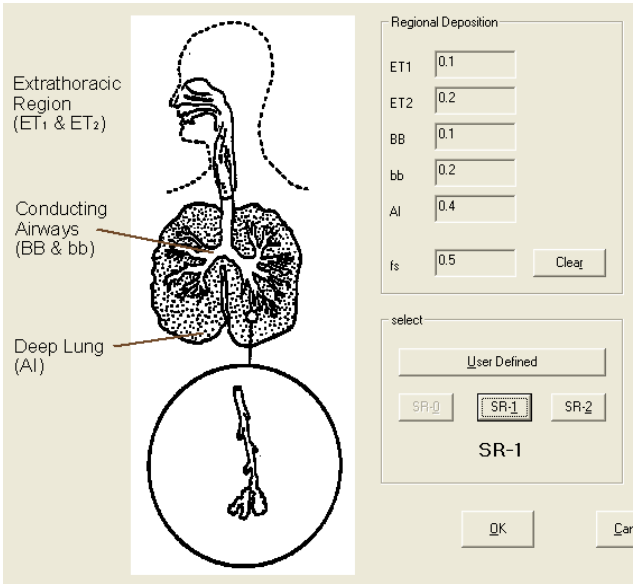


Figure 3.72. Default regional deposition for **Type SR-1 Vapor**.

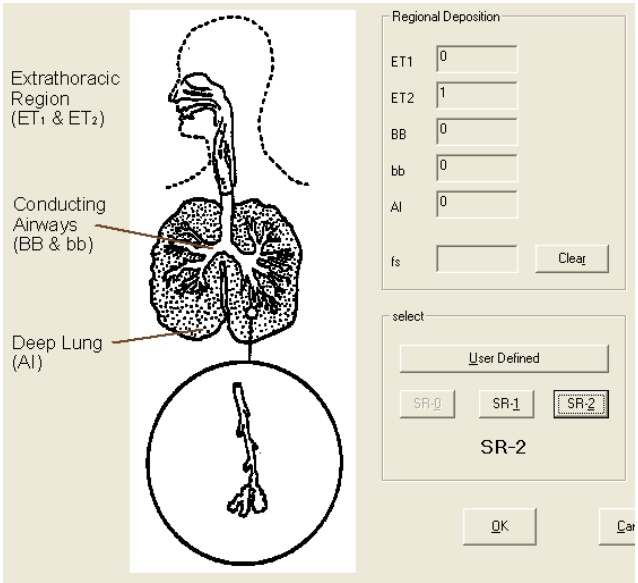


Figure 3.73. Default regional deposition for **Type SR-2 Vapor**.

On *clicking* "**OK**" in the **Vapor Model** window, the *selected* **deposition behavior** is displayed automatically in the **Status Bar** (Figure 3.74).

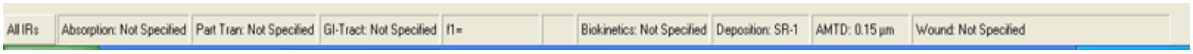


Figure 3.74. Selection of **ICRP Defaults** is automatically indicated on the **Status Bar**.

3.8.2.2. Defining Absorption Behavior

See Section 3.8.4.3. “Absorption Behavior of Vapors”.

3.8.3. Particle Transport Parameters

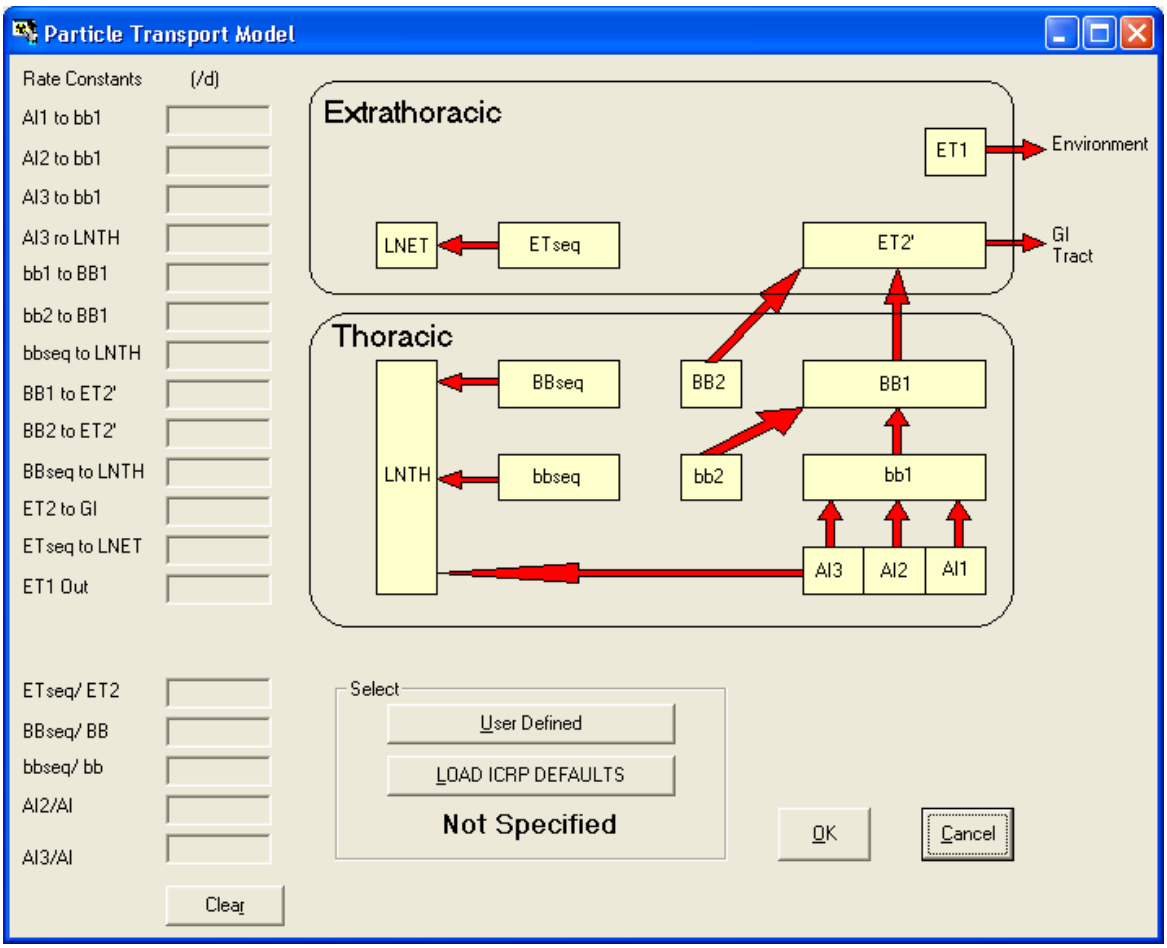


Figure 3.75. Particle Transport Model window.

Clicking the "**Particle Transport**" *button* in the **Model Parameters** sub-panel (**Respiratory Tract** section) displays the **Particle Transport** window (Figure 3.75). *Clicking* the "**LOAD ICRP DEFAULTS**" *button*, followed by the "**OK**" *button*, automatically loads all of the parameter values recommended in *ICRP Publication 66* to represent **Particle Transport** in the respiratory tract of the Reference Worker (Figure 3.76).

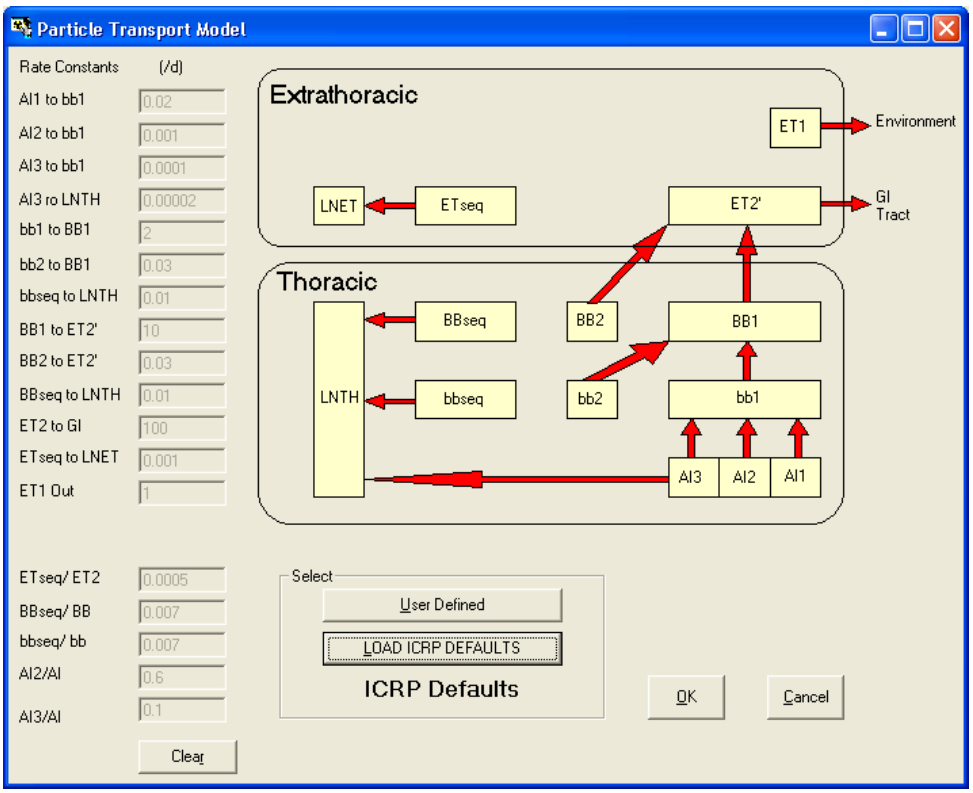


Figure 3.76. Particle Transport Model window loaded with parameter values recommended in *ICRP Publication 66* (**ICRP DEFAULTS**).

Notice that the **ICRP-default** parameter values shown in the **Particle Transport Model** are "greyed-out." These CANNOT be changed. If you wish to define different values, *click* the "**User Defined**" *button*. The **Particle Transport Model** window will then change to that shown in Figure 3.77. This enables you to change the value of ANY **Rate Constant**.

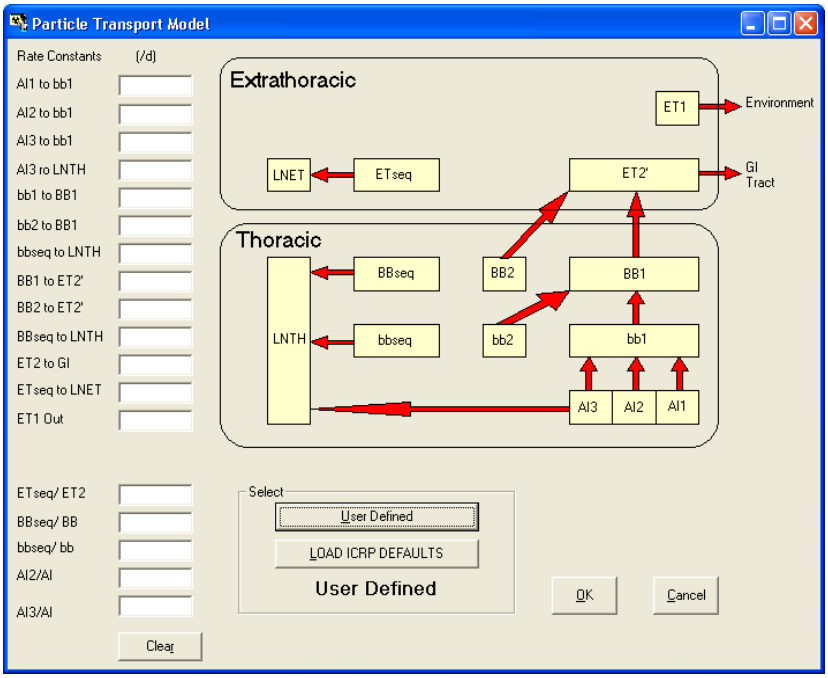


Figure 3.77. Particle Transport Model window in its "**User Defined**" mode.

In the "**User Defined**" mode, all of the initially loaded parameter values are those recommended in ICRP Publication 66. In this mode, you can change as many values as you wish. However, if you change ANY of the ICRP-recommended values, this will be "flagged" automatically in the **Status Bar** as "**Part Tran: User Defined**" (Figure 3.78).

Figure 3.78. Selection of **User Defined** particle transport parameter values is automatically indicated on the **Status Bar**.

Note: If you need to, you can set the values of the particle transport parameters independently for EACH **Intake** by **Inhalation** (*i.e.*, each **IR #**).

Warning: You MUST enter values of particle transport **Rate Constants** in the **Unit** "**d^{-1}**," *i.e.*, "**per day**."

Tip: Appendix A - Technical Basis cites an example in which changing the value of the rate constant of particle transport from **AI3** to **LNTH** (for an individual case) improved the prediction of tissue analysis data (James et al., 2003).

3.8.4. Absorption Parameters

IMBA Expert™ OCAS/ORAU-Edition provides two methods of defining the values of absorption parameters for substitution in the *ICRP Publication 66* respiratory tract absorption model - and the associated value of the gut uptake fraction (f_1).

- Select ICRP-recommended "default" values - using a built-in **data library** compiled from *ICRP Publication* sources;
- Define your own values - utilizing experimental or other data that is "**specific**" to the material involved in the intake.

3.8.4.1. Selecting ICRP Default Absorption Parameters

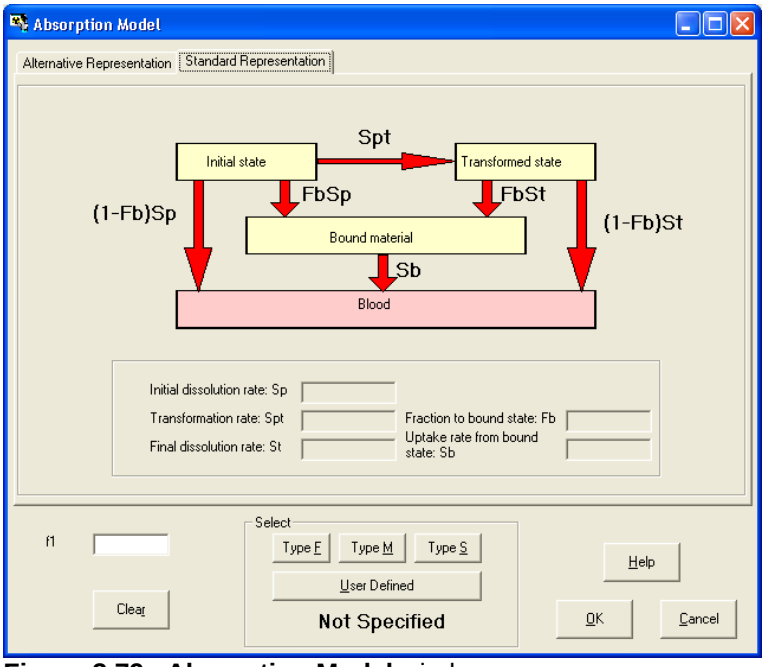


Figure 3.79. Absorption Model window.

Clicking the "**Absorption**" *button* in the **Model Parameters** sub-panel (**Respiratory Tract** section) displays the **Absorption** window (Figure 3.79). This window is used to define BOTH:

- the gut absorption fraction (f_1), and;
- the absorption characteristics for material in the respiratory tract.

Clicking the "**Help**" *button* in this window provides you with information taken from ICRP documents which gives BOTH default absorption rates and f_1 values for different chemical forms of the **Indicator Nuclide**. Figure 3.80 shows the **F1 values for Am** window.

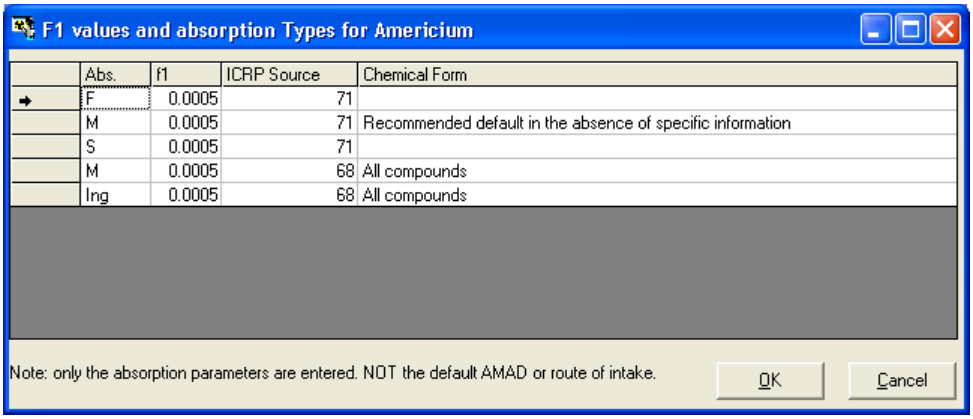

F1 values and absorption Types for Americium
Abs.
f1
ICRP Source
Chemical Form
F 0.0005 71
M 0.0005 71 Recommended default in the absence of specific information
S 0.0005 71
M 0.0005 68 All compounds
Ing 0.0005 68 All compounds
Note: only the absorption parameters are entered. NOT the default AMAD or route of intake.
OK
Cancel

Figure 3.80. F1 values and Absorption Types for Americium window - for **Help** in selecting the value of f_1 for material containing americium.

Note: If you have not previously selected the **Indicator Nuclide**, you CANNOT use the "**Help**" button in the **Absorption Model** window. In this case, IMBA Expert™ OCAS/ORAU-Edition will display a WARNING message - prompting you to *Select* an **Indicator Nuclide**.

You can *select* BOTH the **Absorption Type** and its associated value of f_1 from the **F1 values** window - by *clicking* on any **cell** in the desired **row**, and then *clicking* the "**OK**" *button*. This will load BOTH the selected f_1 value (into the "**f1**" dialog box in the **Absorption Model** window) and the **Absorption Type** - and you will be returned to the **Absorption Model** window.

Tip: If you need to define your own value of f_1, then you can do this directly in the **Absorption Model** window - by typing your specific f_1 value in the "**f1**" dialog box.

Tip: You can also define the value of f_1 in the **GI Tract Model** window. BOTH the **Absorption Model** window and the **GI Tract Model** window display the currently loaded value of f_1 - and this can be modified in EITHER window.

In Figure 3.81, **Absorption Type** "**M**" is selected. *Clicking* the "**OK**" *button* loads the value "**5.00E-04**" (taken from ICRP Publication 71) into the "**f1**" dialog box in the **Absorption Model** window. It also loads the selected ICRP Publication 66 **Absorption Type** ("**M**"), as shown in Figure 3.81. The **Status Bar** will also be updated automatically (Figure 3.82).

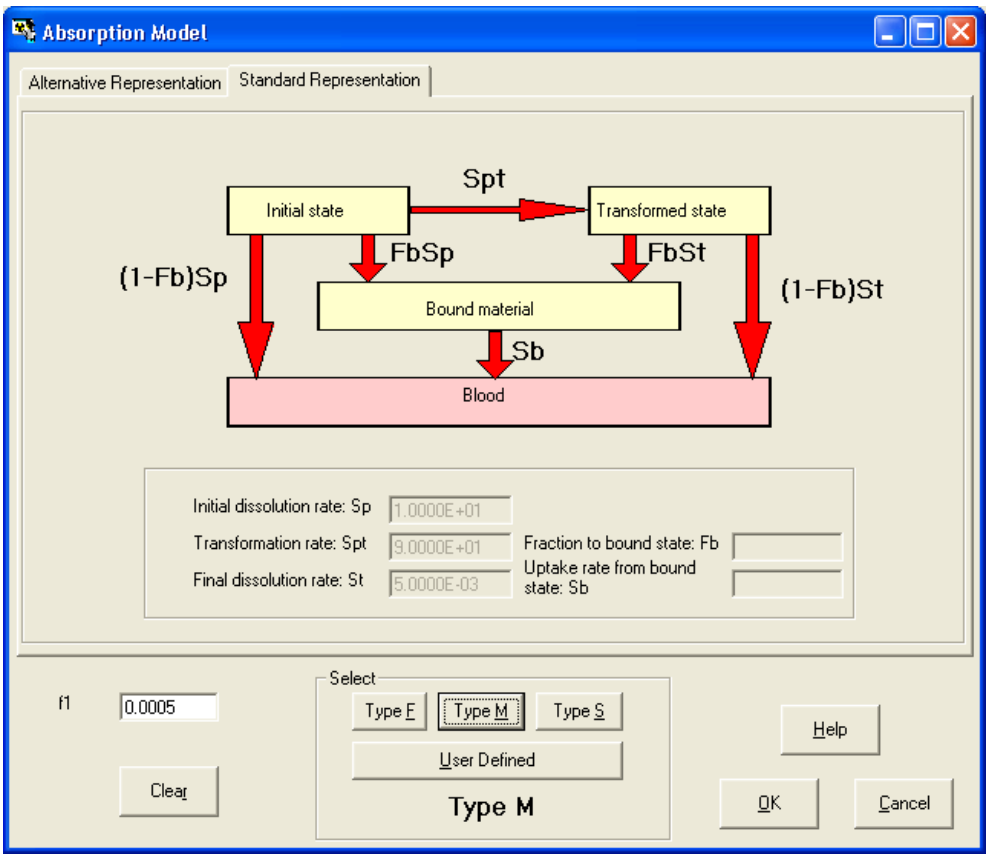


Figure 3.81. Absorption Model window with the *ICRP Publication 71* recommended f_1 value for **Type M** (Americium) loaded.

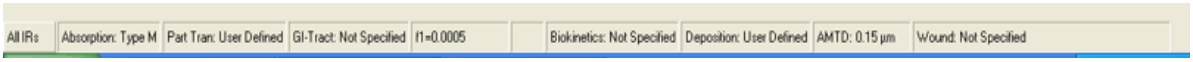


Figure 3.82. The selected **Type M** absorption behavior and the f_1 value is automatically indicated on the **Status Bar**.

You can switch the selection of **ICRP Default Absorption Type** in the "**Absorption Model**" window - by *clicking* another "**Type**" *button*. For example, Figure 3.83 shows the changed parameter values that are displayed when you *click* the "**Type S**" button.

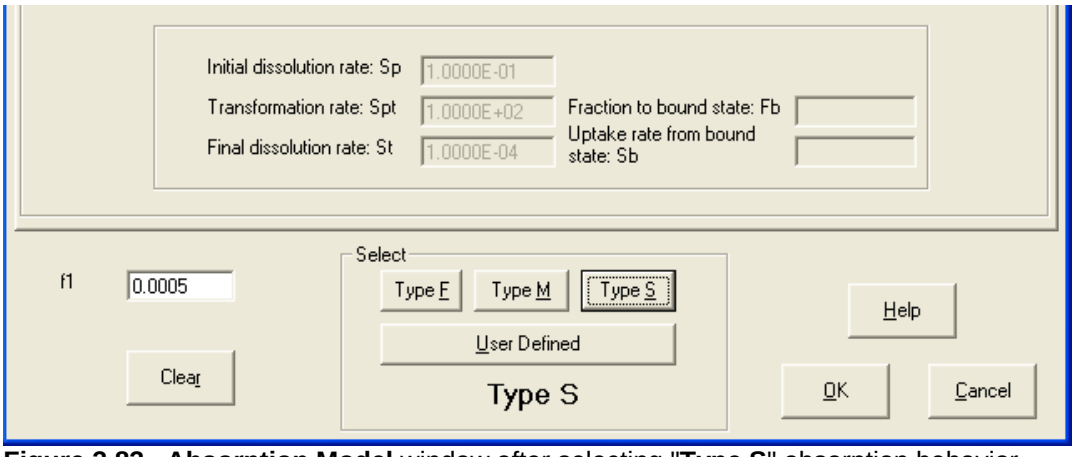


Figure 3.83. Absorption Model window after selecting "**Type S**" absorption behavior.

	Warning: Selecting a different respiratory tract **Absorption Type** does NOT automatically select an appropriate value of the gut absorption factor (f_1). This is YOUR responsibility! The previously-loaded value of f_1 will remain in the "**f1**" dialog box until you **Clear** and/or **replace** this with a new value.
	Tip: It is a good idea to go back and *click* the "**Help**" *button* again - to check out the ICRP-recommended value of f_1 that is appropriate for your newly selected respiratory tract **Absorption Type**.
	Note: Remember that selecting an ICRP default from the "**Help**" button loads BOTH the **Absorption Type** and f_1 value, whereas selecting the **Absorption Type** by *clicking* a "**Type**" *button* will load ONLY the **Absorption Type**.

3.8.4.2. Defining Your Own Absorption Parameters

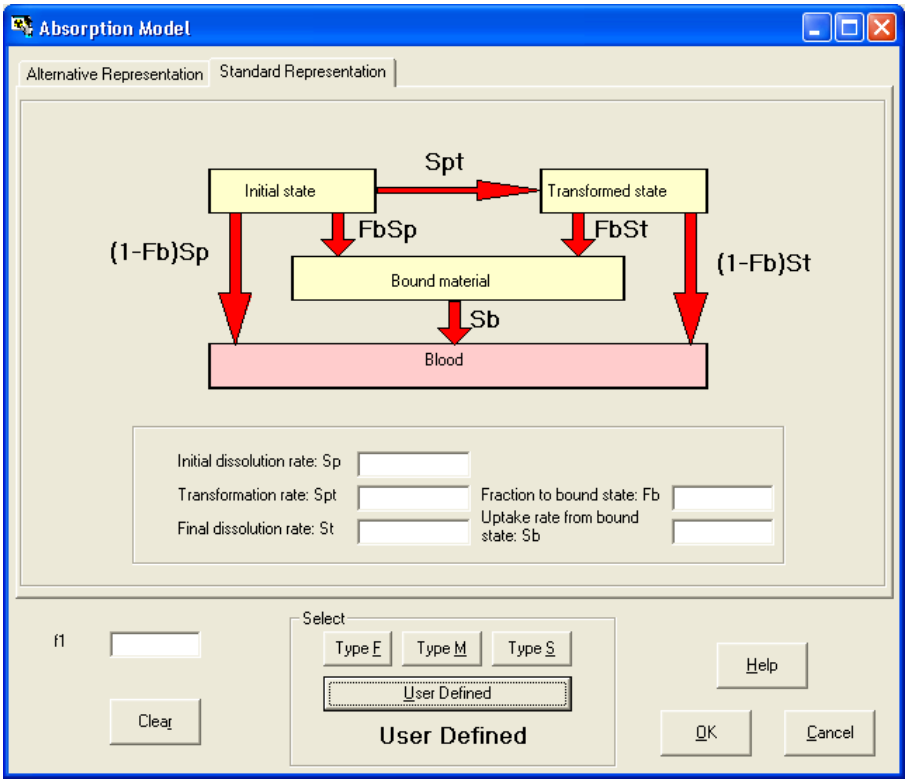


Figure 3.84. Absorption Model window for **User Defined** parameter *option*.

Click the "**User Defined**" button in the **Absorption Model** window to define your own specific values for the respiratory tract **Absorption Parameters** (Figure 3.84). You can then type your required values for the absorption rate constants directly into the respective dialog boxes. These dialog boxes are:

- the **Initial dissolution rate: Sp** (in d^{-1});
- the [particle] **Transformation rate: Spt** (in d^{-1});
- the **Final dissolution rate: St** (in d^{-1});
- the **Fraction to bound state: Fb**;
- the **Uptake rate from bound state: Sb**.

The ICRP Publication 66 respiratory tract absorption model, and these special absorption terms, are described in **Appendix A: Technical Basis**, Section A.4.4. – "**Model of Material Absorption**").

Key Tip: Throughout IMBA Expert™ OCAS/ORAU-Edition, dialog boxes in which you can ***type*** a value directly are indicated by a *white* background. A "*greyed*" box indicates a value that CANNOT be changed (in the current window setting).

Figure 3.85 shows a hypothetical example of absorption rates that might be entered for an extremely insoluble material, *i.e.*, a material that dissolves and is absorbed **more slowly** than the ICRP default **Type S**. Also in this hypothetical example, it is assumed that **5%** of the radionuclide activity that is **dissolved** (from the particles) is "**bound**" temporarily to respiratory tract tissues - to be released into the blood at the rate of $\mathbf{10^{-3}\ d^{-1}}$. The hypothetical values of the absorption parameters are:

- $\mathbf{s_p} = 10^{-2}\ d^{-1}$;
- $\mathbf{s_{pt}} = 100\ d^{-1}$;
- $\mathbf{s_t} = 10^{-5}\ d^{-1}$;
- $\mathbf{f_b} = 0.05$;
- $\mathbf{s_b} = 10^{-3}\ d^{-1}$.

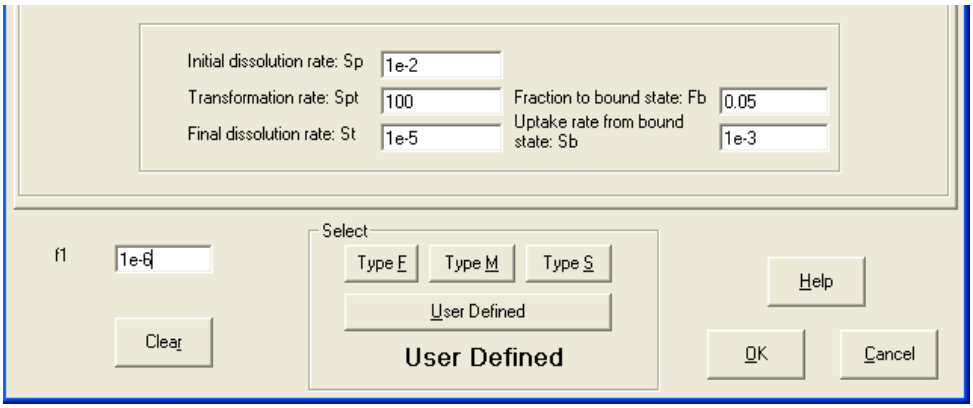


Figure 3.85. ***Entering*** your own (non-default) values of **Absorption Rates.**

Warning: The **Unit** in which **Absorption Rates** are expressed in IMBA Expert™ OCAS/ORAU-Edition is ALWAYS "$\mathbf{d^{-1}}$," *i.e.*, "**per day**." You MUST enter your **values** in the same **Unit** ("$\mathbf{d^{-1}}$").

IMBA Expert™ OCAS/ORAU-Edition implements both representations of particle dissolution and absorption of material from the respiratory tract that were recommended in ICRP Publication 66:

- the "**Standard Representation**" - as shown in Figure 3.85;
- the "**Alternative Representation**."

Figure 3.86 shows the **Alternative Representation** of the hypothetical particle dissolution, radionuclide binding, and absorption characteristics listed above (for comparison with the **Standard Representation** shown in Figure 3.85). IMBA Expert™ OCAS/ORAU-Edition automatically calculates the mathematical transformation between these two representations. As

described in **Appendix A: Technical Basis**, Section A.4.4. – "**Model of Material Absorption**"), these two representations of the dissolution and absorption processes give identical results.

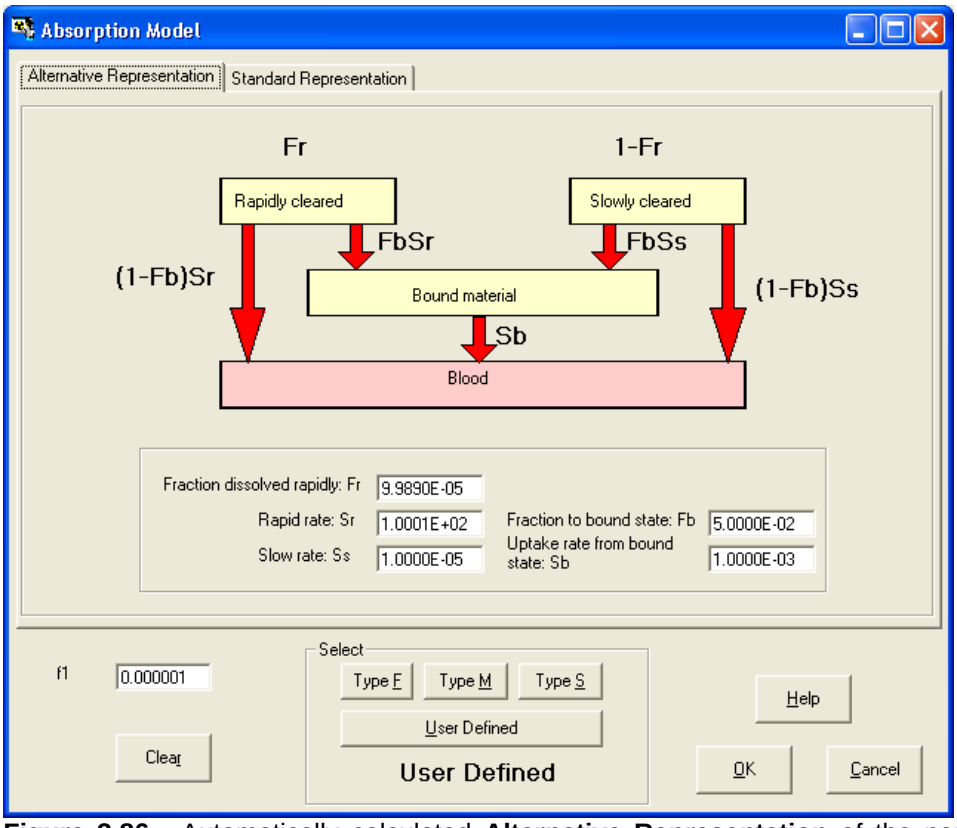


Figure 3.86. Automatically calculated **Alternative Representation** of the particle dissolution, material binding and absorption characteristics shown in Figure 3.85.

The alternative dissolution and absorption parameters are:

- **Fraction dissolved rapidly, f_r** = 9.9890×10^{-5};
- **Rapid rate, s_r** = $100.01\ d^{-1}$;
- **Slow rate, s_s** = $10^{-5}\ d^{-1}$;
- **Fraction to bound state, f_b** = 5×10^{-2};
- **Uptake rate from bound state, s_b** = $10^{-3}\ d^{-1}$.

Both representations of the particle dissolution and material absorption processes have their practical uses. The **Standard Representation** is helpful when a physical process (such as particle fragmentation) leads to the gradual transformation of deposited particles into a more soluble form, *i.e.*, in cases where the overall absorption rate *increases* with time - see **Technical Basis** for an example of this. The **Alternative Representation** is useful for the more general situation, where the overall absorption rate *decreases* with time. For example, *in vitro* solubility studies are usually interpreted in terms of "fast" and "slow" dissolution fractions, with their associated dissolution rates. Such results can be substituted directly in the **Alternative Representation** (Figure 3.86).

3.8.5. Absorption Behavior of Vapors

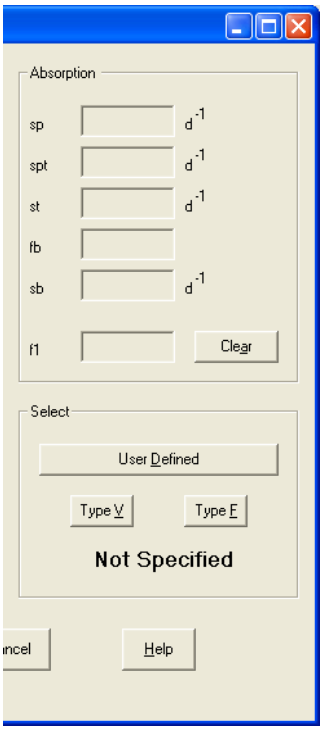


Figure 3.87. Absorption panel in the **Vapor Model** window.

The absorption behavior of a vapor is defined in the "**Absorption**" panel of the **Vapor Model** window (Figure 3.87). *Clicking* the "**Type V**" button displays the values of absorption parameters and gut uptake fraction (f_1) shown in Figure 3.88, for **Type V** absorption behavior (ICRP 2002b).

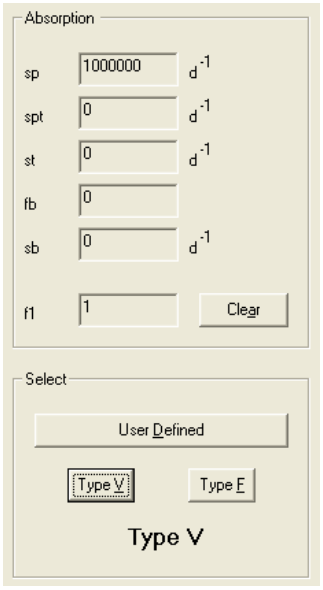


Figure 3.88. Absorption parameters and f_1 value for a **Type V** vapor.

The displayed values of absorption parameters and f_1 are read into IMBA Expert™ OCAS/ORAU-Edition by clicking the "**OK**" button (in the **Vapor Model** window). The selected **Absorption Type** and f_1 value will then be displayed in the **Status Bar** (Figure 3.89).

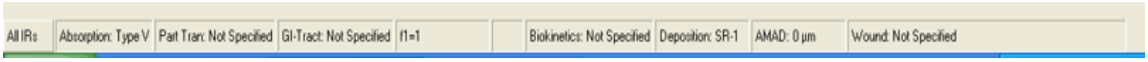


Figure 3.89. The selected **Type V** absorption behavior and the f_1 value is automatically indicated on the **Status Bar**.

Clicking the "**Type F**" button displays the values of absorption parameters and f_1 shown in Figure 3.90, for **Type F** absorption behavior (ICRP 1994a).

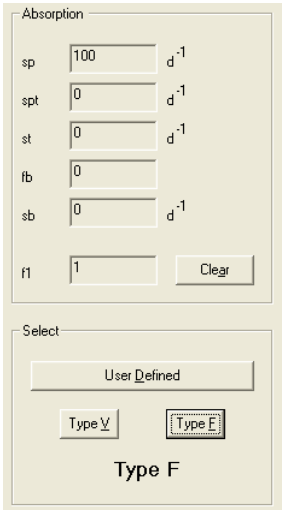


Figure 3.90. Absorption parameters and f_1 value for a **Type F** vapor.

3.8.6. Wound Model – Generic

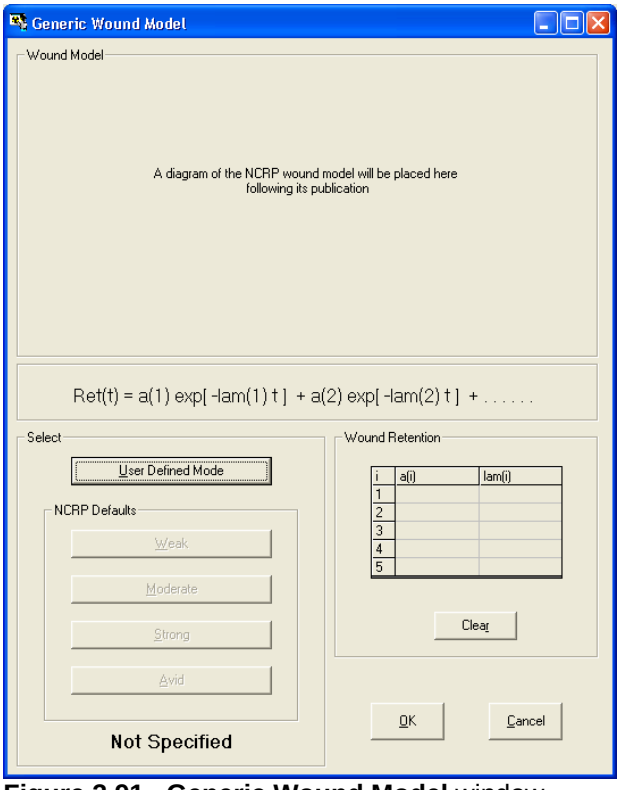


Figure 3.91. Generic Wound Model window.

Selecting "**Wound**" as the **Intake Scenario** (in the **Main Screen**) automatically *highlights* the "**Wound**" model button. *Clicking* the "**Wound**" model button opens the "**Generic Wound Model**" window (Figure 3.91). This enables parameters to be defined to represent wound retention and systemic uptake - by clicking the "**User Defined Mode**" button (Figure 3.92).

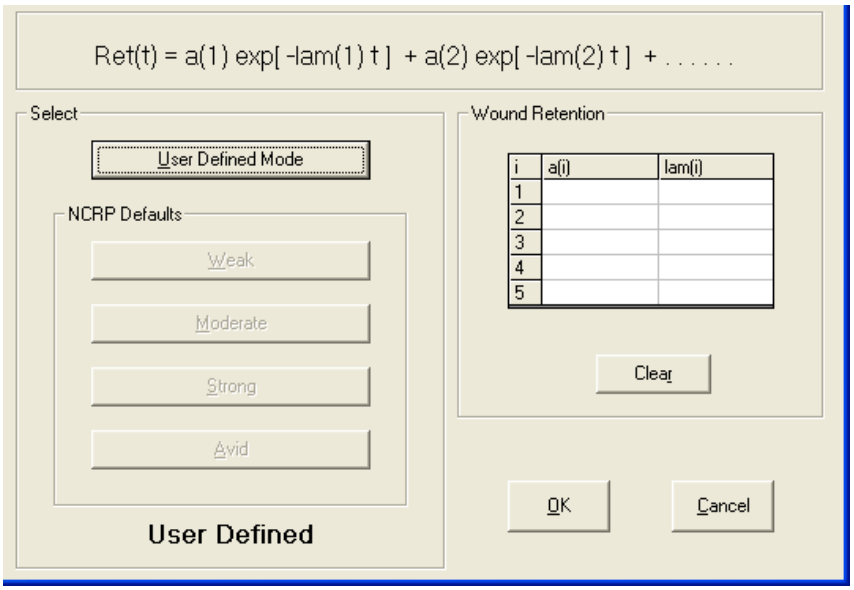


Figure 3.92. Defining a **Retention Function** for a **Wound** (transdermal intake).

3.8.7. GI-Tract Retention Parameters

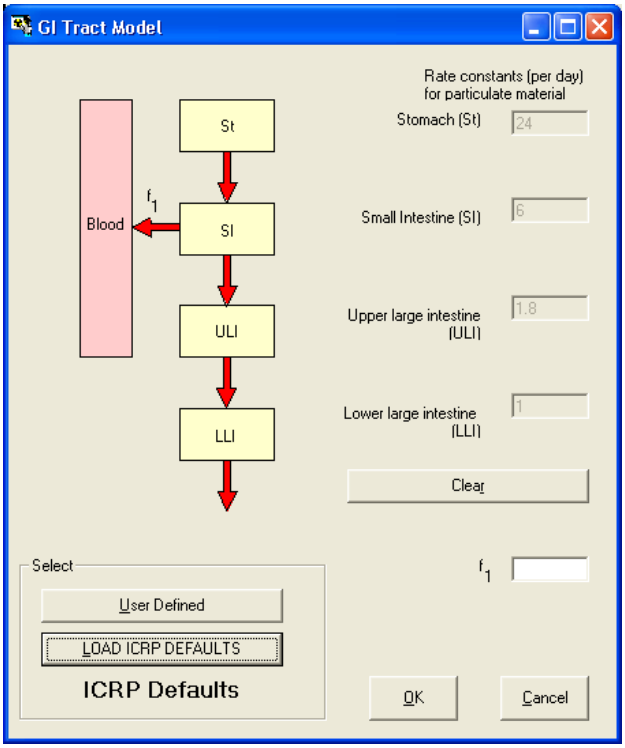


Figure 3.93. The *ICRP Publication 30* **GI Tract Model** with **ICRP Default** parameter values loaded.

If, for a particular **Intake Regime (IR)** you have selected either **Inhalation** or **Ingestion**, then the "**GI-Tract**" *button* in the "**Model Parameters**" sub-panel is *enabled* automatically). *Click* the "**GI-Tract**" *button* to display the **GI Tract Model** window. *Click* the "**LOAD ICRP DEFAULTS**" *button* in this window to load the ICRP-recommended parameter values (Figure 3.93).

In Figure 3.93, the "$\mathbf{f_1}$" dialog box is displaying the value of "**0.0005**" for the gut absorption fraction (f_1). If you had selected the f_1 value earlier, *e.g.*, in the **F1 Values** window and/or the **Absorption Model** window (see Selecting ICRP Default Parameters), then the same f_1 value would have been loaded automatically in the "$\mathbf{f_1}$" dialog box. If, however, you had loaded a **New** (blank) **Parameter File**, and proceeded directly to set up the parameters for an **Ingestion** intake, the "$\mathbf{f_1}$" dialog box would have appeared empty. In either case, you can type a new value of f_1 directly into the "$\mathbf{f_1}$" dialog box (Figure 3.93).

To "look up" an appropriate ICRP-default value of f_1, *click* the "**Help**" button in the **GI Tract Model** window. This will *open* the "**F1 Values**" window for the currently selected **Indicator Nuclide** (Figure 3.94) - from which you can *select* your f_1 value.

	Note: The f_1 "**Help**" *button* only appears in the **GI Tract Model** window IF you have selected "**Ingestion**" as the **Route** of intake.
	Note: In the f_1 "**Help**" window, *indicate* a **row** displaying your desired f_1 value, and then *click* "**OK**." ONLY the displayed f_1 value will be **loaded**. The associated respiratory tract absorption type (**Abs. Type**) is NOT loaded - since this is irrelevant for the intake by **Ingestion**.

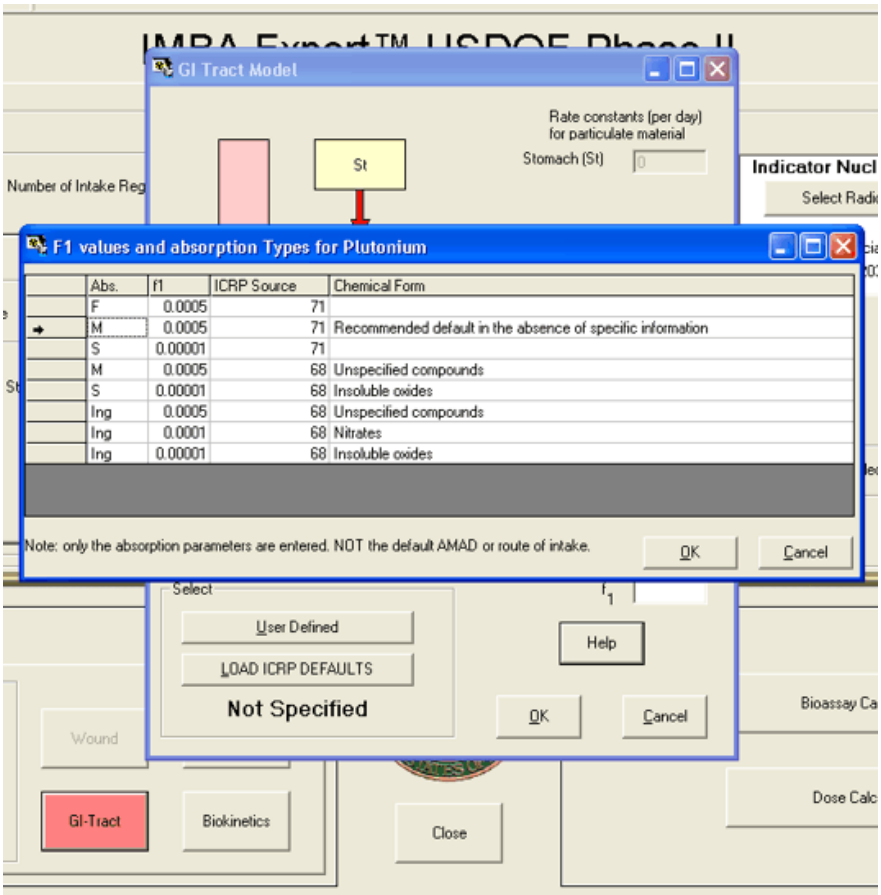

GI Tract Model
Rate constants (per day) for particulate material
Stomach (St)
St
Indicator Nucl
Select Radi
F1 values and absorption Types for Plutonium
Abs. | f1 | ICRP Source | Chemical Form
F | 0.0005 | 71 |
M | 0.0005 | 71 | Recommended default in the absence of specific information
S | 0.00001 | 71 |
M | 0.0005 | 68 | Unspecified compounds
S | 0.00001 | 68 | Insoluble oxides
Ing | 0.0005 | 68 | Unspecified compounds
Ing | 0.0001 | 68 | Nitrates
Ing | 0.00001 | 68 | Insoluble oxides
Note: only the absorption parameters are entered. NOT the default AMAD or route of intake.
OK
Cancel
Select
User Defined
LOAD ICRP DEFAULTS
Not Specified
Help
OK
Cancel
Wound
Bioassay Ca
Dose Calc
GI-Tract
Biokinetics
Close

Figure 3.94. The **F1 values and absorption Types for Plutonium** window.

Note: If you have *un-checked* the option to "**Apply Model Params to All IRs**" (in the **Advanced** menu), then you can assign a different f_1 value for each **IR** - see "Setting Up Models for Each IR."

IMBA Expert™ OCAS/ORAU-Edition also enables you to define your own values for the **GI-tract transport rate constants**. *Click* the "**User Defined**" button in the **GI Tract Model** window. All dialog boxes will then appear with a white background (Figure 3.95) - ready for you to type in your new values.

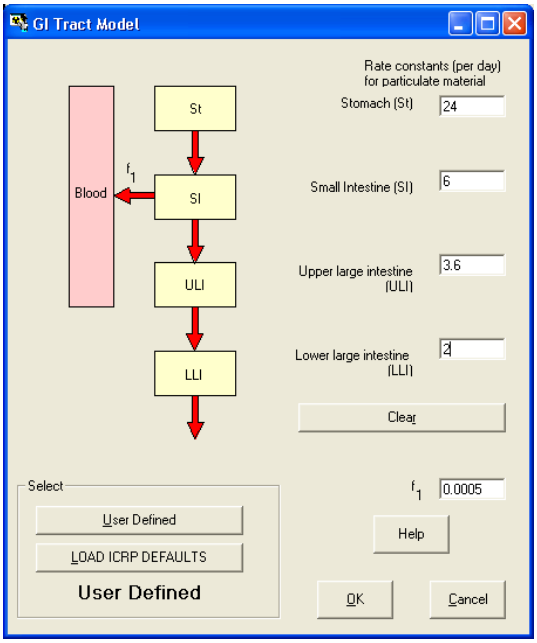


Figure 3.95. The **GI Tract Model** in the "**User Defined**" mode.

3.8.8. Bioassay Parameters

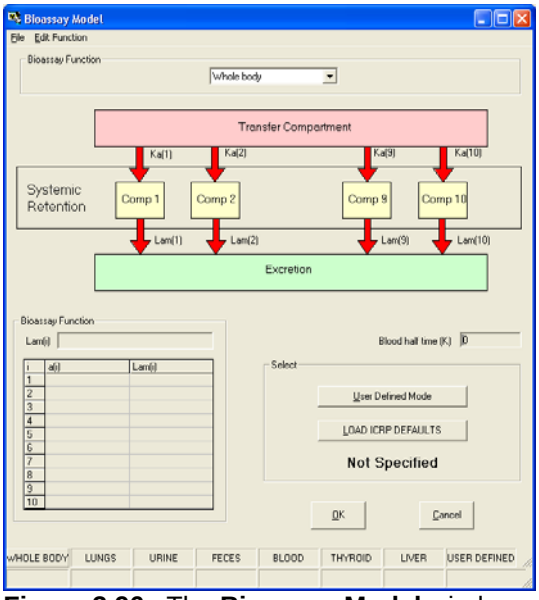


Figure 3.96. The **Bioassay Model** window.

Click the "**Bioassay**" *button* in the "**Model Parameters**" sub-panel to display the Bioassay Model (Figure 3.96). If you have previously selected the Indicator Nuclide, this window enables you to select (or define) all of the required bioassay functions. *Click* the down arrow on the **Bioassay Function** list box to see the drop-down list of bioassay *options* (Figure 3.97).

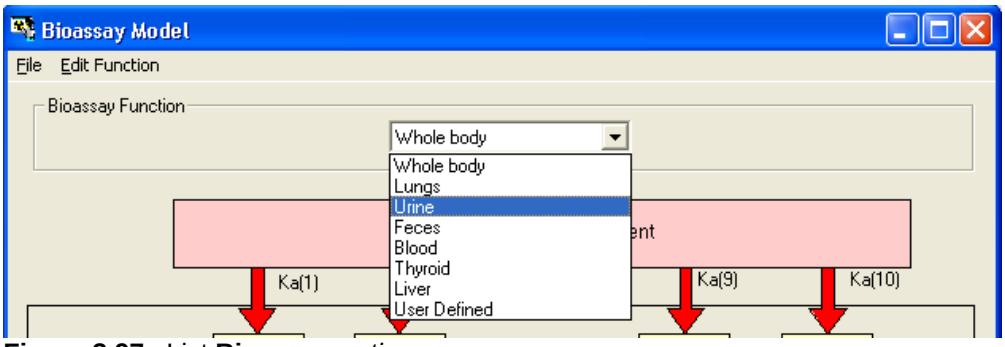


Figure 3.97. List **Bioassay** *options*.

Highlight and *click* your required bioassay *option*. In this example, selection of **urine** changes the **Bioassay Model** window to that shown in Figure 3.98.

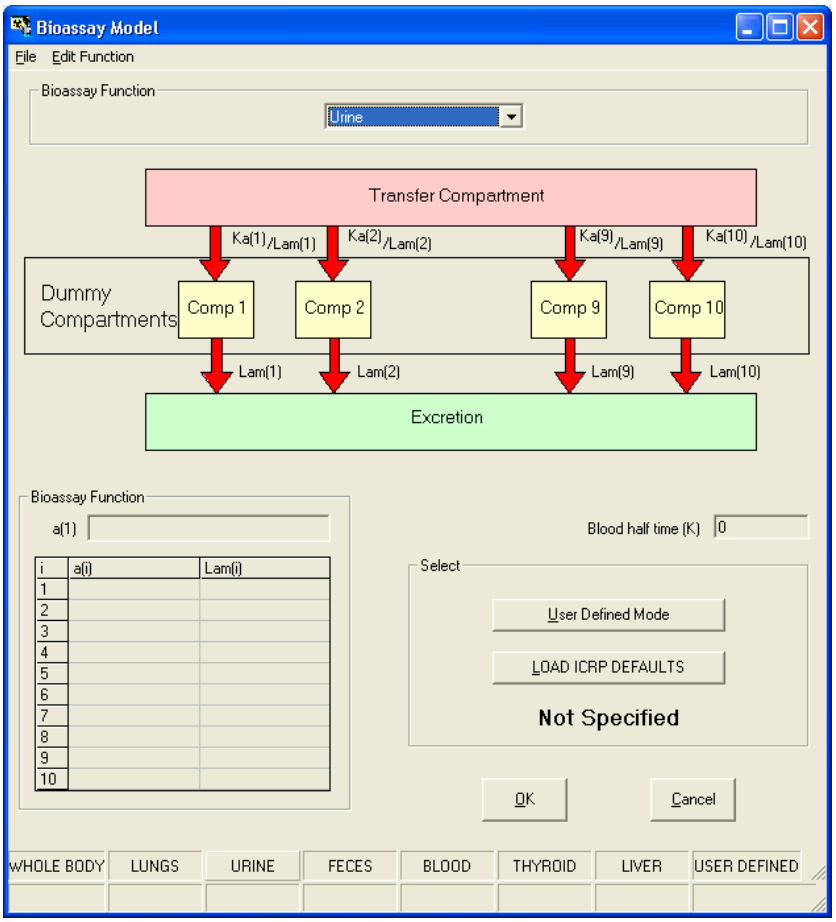


Figure 3.98. Selecting **Urine** in the **Bioassay Model** window.

Notice that the "**URINE**" indicator button is now "*raised*." As yet, however, the Bioassay Function is **Not Specified**. You have two *options* to specify this:

- **User Defined Mode**;
- **LOAD ICRP DEFAULTS**.

3.8.8.1. "LOAD ICRP DEFAULTS" Option

If you *click* the **LOAD ICRP DEFAULTS** *button*, the window will display the parameters of the selected **Bioassay Function** (Figure 3.99). In this case, the function is for **plutonium** in **urine**. This was fitted to the *ICRP Publication 67* plutonium biokinetic model's predictions of plutonium excretion in urine after injection of unit activity into the blood (see **Appendix A: Technical Basis** section A.8.5.4 entitled "**Mathematical Representation of Excretion**").

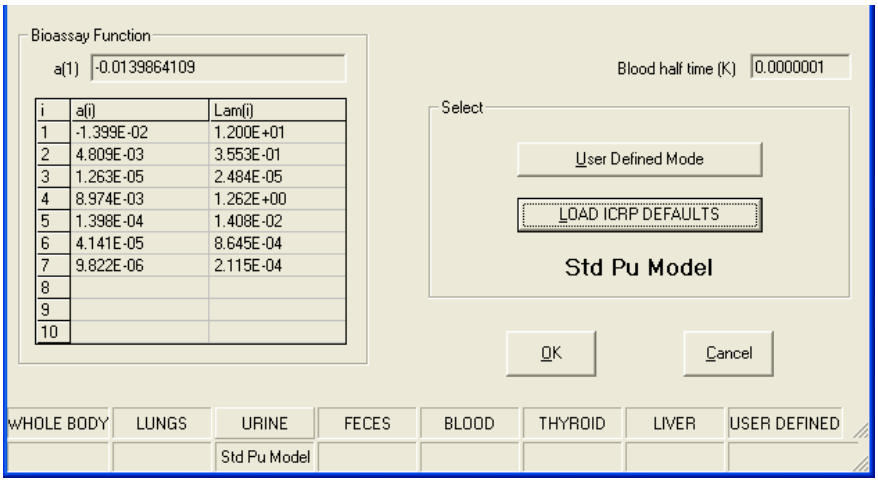


Figure 3.99. Loading the **parameters** of the **Bioassay Function** for **Pu-in-urine**.

Notice that the label "**Std Pu Model**" is now shown under the "**URINE**" indicator button, and also under the "**LOAD ICRP DEFAULTS**" *button*. If you then go back to the **Bioassay Function** drop-down list, *select* "**Feces**," and *click* the "**LOAD ICRP DEFAULTS**" *button* again - then the displayed parameters will change to those shown in Figure 3.100.

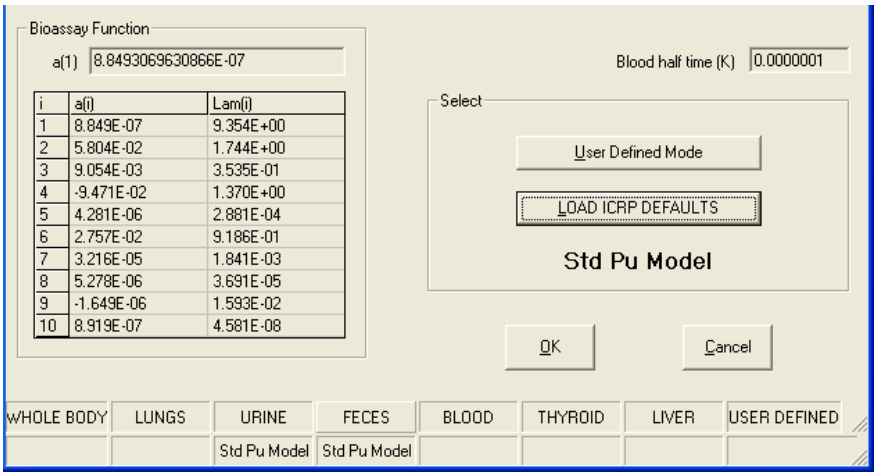


Figure 3.100. Adding the **parameters** of the **Bioassay Function** for **Pu-in-feces**.

Notice that BOTH the "**URINE**" and "**FECES**" indicator buttons are now labeled "**Std Pu Model**." If you try to *load* a "**Thyroid**" **Bioassay Function** (for plutonium), then the **Not Specified** label shown in Figure 3.101 will be displayed. IMBA Expert™ OCAS/ORAU-Edition "knows" that the thyroid is not included specifically in the ICRP Publication 67 biokinetic model for plutonium, and therefore does NOT have a **Bioassay Function**.

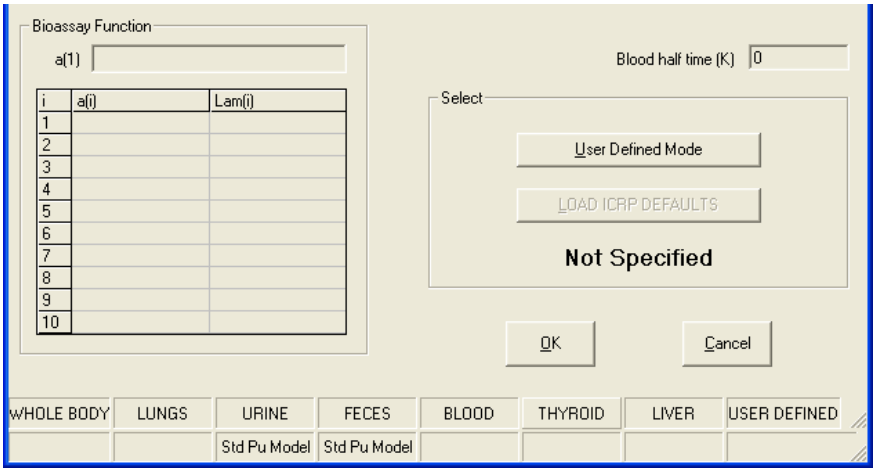


Figure 3.101. Label displayed if you try to load an "ICRP" **Bioassay Function** for **Pu-in-thyroid**.

Similarly, if you try to *load* a **Bioassay Function** for the **Lungs**, then IMBA Expert™ OCAS/ORAU-Edition reminds you that "**No systemic model is required for the lungs**" (Figure 3.102) - since **lung retention** is calculated automatically (using the *ICRP Publication 66* respiratory tract model).

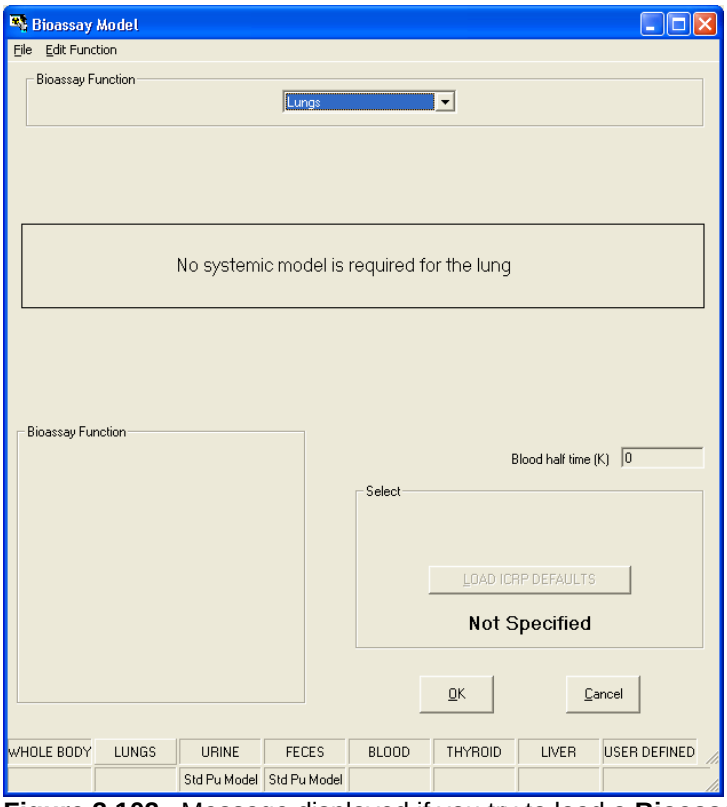


Figure 3.102. Message displayed if you try to load a **Bioassay Function** for the **Lungs**.

The selected **Bioassay Functions** are NOT indicated in the **Status Bar** (Figure 3.103). However, they ARE recorded in the **Parameter File** for your case study.

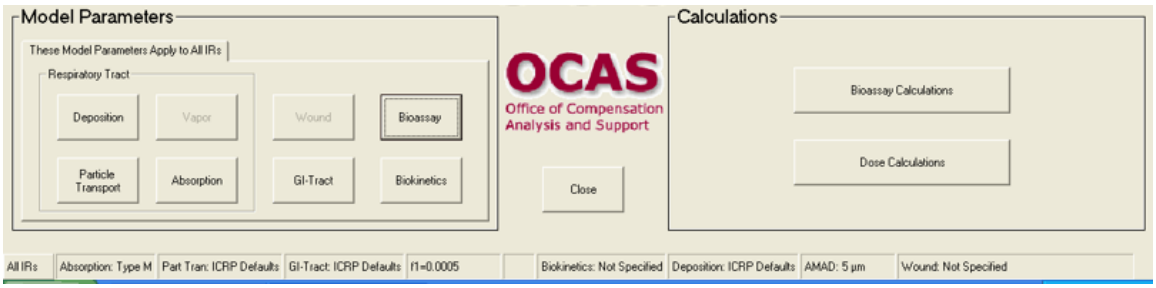


Figure 3.103. The Status Bar does NOT indicate the selected **Bioassay Functions**.

3.8.8.2. "User Defined Mode"

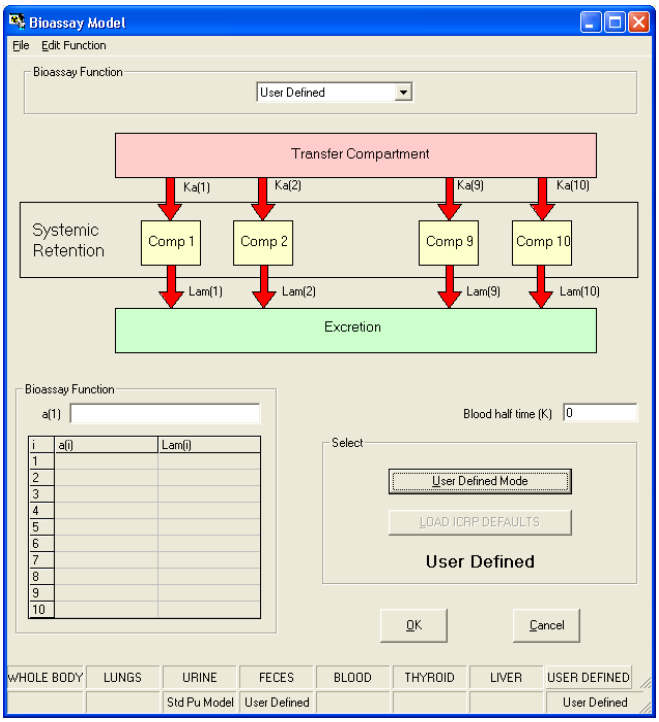


Figure 3.104. The **Bioassay Model** window in the "**User Defined Mode**."

IMBA Expert™ OCAS/ORAU-Edition also enables you to define and use your own **Bioassay Function** - see discussion in the **Technical Basis** on how this should be done. You can set up an additional function (to represent an additional **Bioassay Quantity**, *e.g.*, "**SKELETON**") under the eighth **Bioassay Function** indicator button (labeled "**USER DEFINED**"). You can also *define* and *load* your own **Bioassay Function** (in place of the "**ICRP DEFAULT**") for any of the seven **Bioassay Quantities** that are specified in IMBA Expert™ OCAS/ORAU-Edition.

Warning: If you substitute a different **Bioassay Function** for any **Bioassay Quantity** in IMBA Expert™ OCAS/ORAU-Edition, then any **Dose Calculations** that you perform with ICRP-recommended "**Default**" **Biokinetic Models** may be INCONSISTENT with your **bioassay analyses**. For **Dose Calculations**, IMBA Expert™ OCAS/ORAU-Edition solves all **Biokinetic Models** simultaneously, and so altering the **Biokinetic Model** for a major organ of uptake will affect the amount of radionuclide taken up by **other organs**.

3.8.8.3. "Quick-Loading" All ICRP-Default Bioassay Functions

As an alternative to defining and loading each **Bioassay Function** separately, IMBA Expert™ OCAS/ORAU-Edition enables you to "***Quick-Load***" the bioassay functions for ALL *ICRP-recommended* **Bioassay Models** with a single *click* – see Section 3.8.10. "**One-step Loading of All Model Parameters**".

3.8.9. Biokinetic Parameters

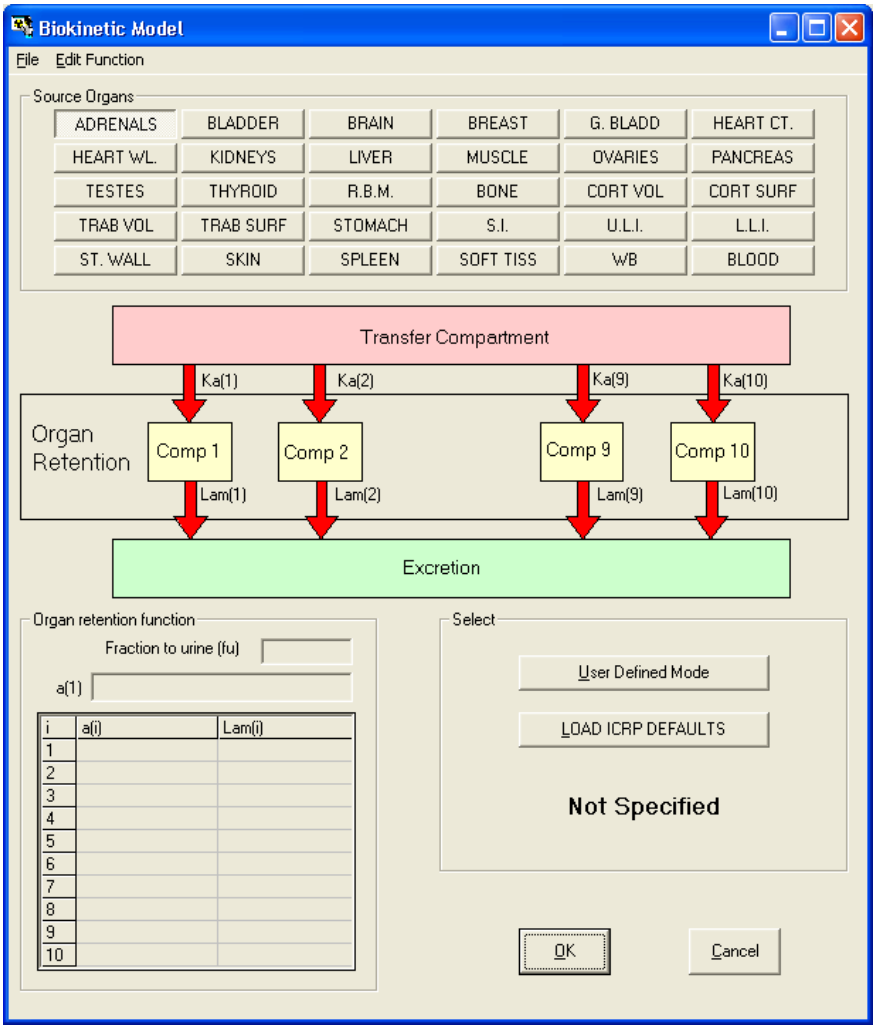


Figure 3.105. The **Biokinetic Model** window.

Click the "**Biokinetics**" button in the "**Model Parameters**" sub-panel to open the Biokinetic Model window (Figure 3.105). If you have previously selected the Indicator Nuclide, this window enables you to "**LOAD ICRP DEFAULTS**," i.e., select all of the required source region (source organ or tissue) retention functions.

Warning: If you have NOT previously selected the **Indicator Nuclide**, then the **LOAD ICRP DEFAULTS** *button* will be "*greyed out*" - and you will NOT be able to use this to load an "*ICRP*" model for a selected "**Source Organ**."

3.8.9.1. "LOAD ICRP DEFAULTS" option

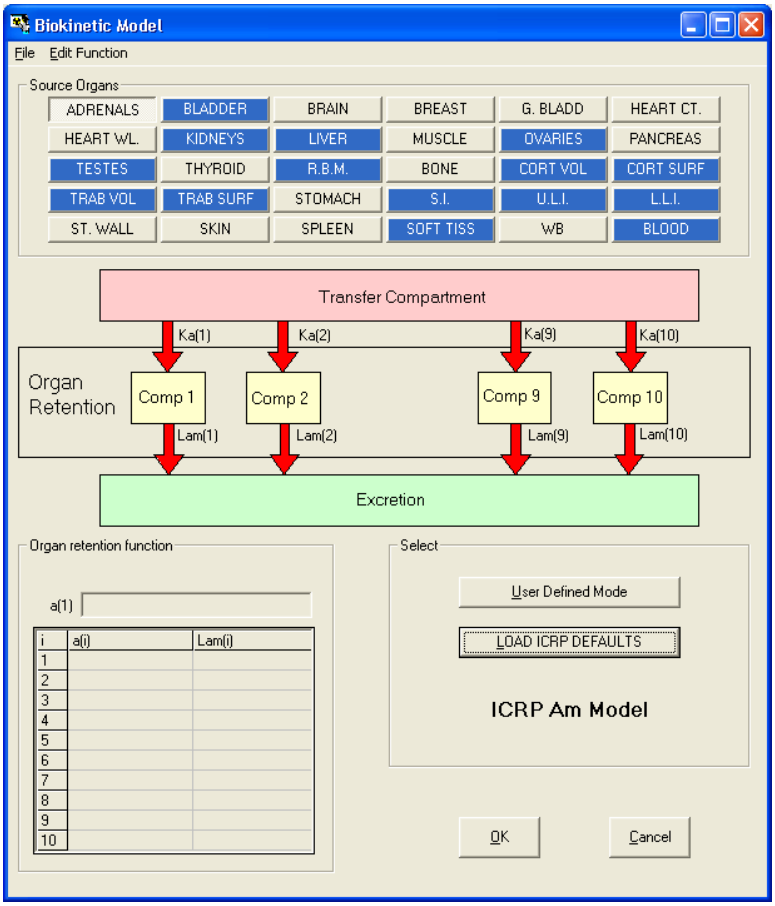

Biokinetic Model
File Edit Function
Source Organs
ADRENALS BLADDER BRAIN BREAST G. BLADD HEART CT.
HEART WL. KIDNEYS LIVER MUSCLE OVARIES PANCREAS
TESTES THYROID R.B.M. BONE CORT VOL CORT SURF
TRAB VOL TRAB SURF STOMACH S.I. U.L.I. L.L.I.
ST. WALL SKIN SPLEEN SOFT TISS WB BLOOD
Transfer Compartment
Ka(1) Ka(2) Ka(9) Ka(10)
Organ Retention
Comp 1 Comp 2 Comp 9 Comp 10
Lam(1) Lam(2) Lam(9) Lam(10)
Excretion
Organ retention function
a(1)
i a(i) Lam(i)
1 2 3 4 5 6 7 8 9 10
Select
User Defined Mode
LOAD ICRP DEFAULTS
ICRP Am Model
OK
Cancel

Figure 3.106. Loading the **ICRP Default** Biokinetic Models for americium.

Clicking the **LOAD ICRP DEFAULTS** *button* automatically loads the fitted retention functions that represent the complete set of ICRP-default **Biokinetic Models** - for your selected **Indicator Nuclide**. The **Source Organs** involved are automatically *highlighted* in the **Biokinetic Model** window (Figure 3.106). You can examine the **retention function** loaded for any *highlighted* **Source Organ** by *clicking* its *indicator button*. For example, Figure 3.107 shows the retention function loaded for "**Liver**" - which represents liver uptake and retention of americium according to the ICRP Publication 67 **Biokinetic Model**.

When the "**Liver**" retention function is displayed in the **Biokinetic Model** window, the "**Liver**" **indicator button** is shown "*depressed*." *Selecting* another **Source Organ** will "*release*" the "*Liver*" *indicator button*, "*depress*" the button for the newly selected **Source Organ**, and display its **retention function**.

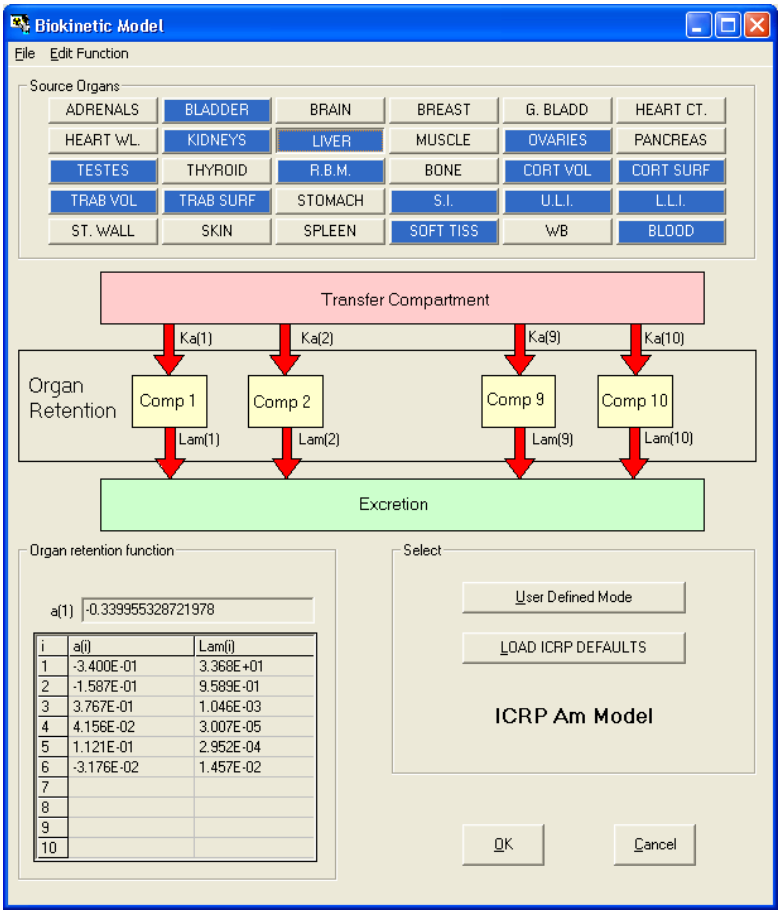


Figure 3.107. The **retention function** for americium in liver.

Figure 3.108. The **Status Bar** indicates that the **ICRP Am Model** for "**Biokinetics**" has been loaded.

The fact that the **complete** ICRP-default biokinetic model has been loaded is indicated automatically in the **Status Bar** (Figure 3.108).

3.8.9.2. "User Defined Mode"

You can *select* the "**User Defined Mode**" to replace one or more **retention functions** with your own parameter values. The **Biokinetic Model** window displaying the "*ICRP*" retention function for americium in "**Liver**" (Figure 3.107) changes to that shown in Figure 3.109 when you *click* the "**User Defined Mode**" *button*.

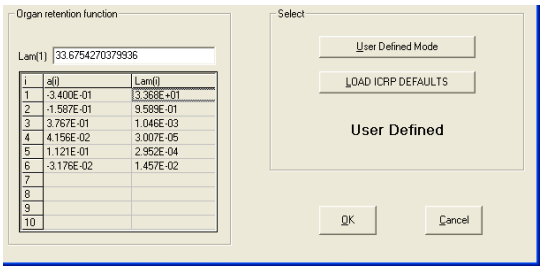


Figure 3.109. The "**User Defined Mode**" for re-defining the **retention function** for americium in liver.

In this mode, the parameter values representing the ICRP-default **Biokinetic Model** are initially retained, but the "**Organ retention function**" display becomes a *dialog box* (with a *white* background). You can now *select* the parameter that you want to change, and *type* your new value into the *dialog box* [see Figure 3.109, where the parameter "Lam(1)" has been *selected*]. Your new **retention function** can have up to **ten** exponential terms (see **Appendix A: Technical Basis**). Once you have *selected* the **User Defined Mode**, the **Status Bar** will indicate this (Figure 3.110) - even if you make no change to an "*ICRP-default*" parameter value.

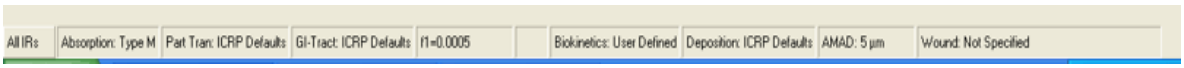


Figure 3.110. The **Status Bar** indicates that the **User Defined Mode** for "**Biokinetics**" has been selected.

Tip: You can re-load ALL of the "ICRP-default" parameter values by *re-clicking* the "**LOAD ICRP DEFAULTS**" *button*. This will re-set the **Status Bar** *indicator* - to confirm that ALL **ICRP DEFAULT Biokinetic Model** parameter values have been re-loaded.

Warning: If you substitute a different Source Organ **retention function** for any "*ICRP-default*" **Bioassay Model** in IMBA Expert™ OCAS/ORAU-Edition, then the **Dose Calculations** that you perform may NOT be valid for ALL Source/Target Organ combinations. IMBA Expert™ OCAS/ORAU-Edition solves all **Biokinetic Models** simultaneously, and so altering the **Biokinetic Model** for a major organ of uptake will affect the amount of radionuclide taken up by **other source organs**.

3.8.10. One-step Loading of All Model Parameters

3.8.10.1. ICRP-recommended Parameter Values

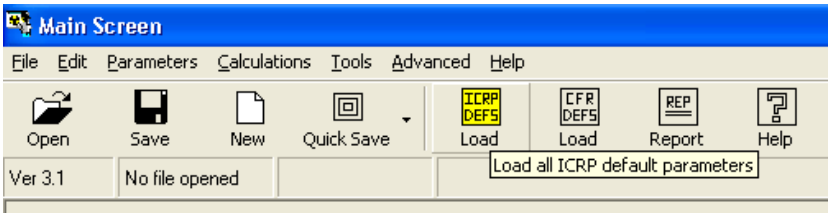


Figure 3.111. The "**ICRP DEFS Load**" *tool button*.

If you *move* your *mouse pointer* over the "**ICRP DEFS Load**" *button* in the **Tool Bar**, the "**ICRP DEFS**" symbol will change color - to *yellow* (Figure 3.111). *Clicking* the *button* will then display the "**F1 values**" window for the selected radioelement (Figure 3.112).

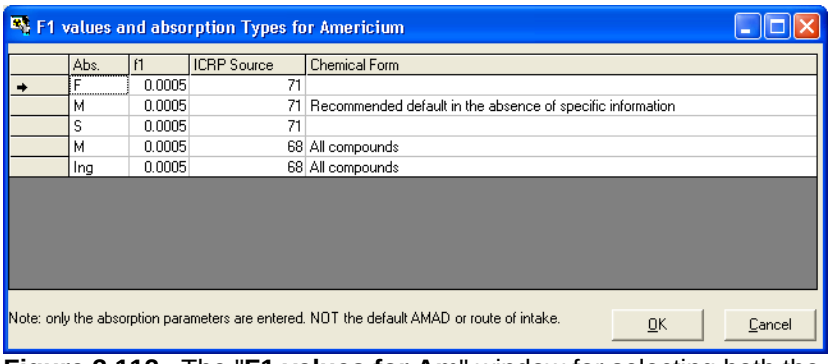

F1 values and absorption Types for Americium
Abs.
f1
ICRP Source
Chemical Form
F 0.0005 71
M 0.0005 71 Recommended default in the absence of specific information
S 0.0005 71
M 0.0005 68 All compounds
Ing 0.0005 68 All compounds
Note: only the absorption parameters are entered. NOT the default AMAD or route of intake.
OK
Cancel

Figure 3.112. The "**F1 values for Am**" window for selecting both the **Absorption Type** and f_1 value for americium.

Select the **row** with your required combination of ICRP-default **Absorption Type** and f_1 value - and *click* "**OK**." This will close the "**F1 values**" window. If you now *click* on the **Bioassay Model** button (**Main Screen**), the **Bioassay Model** window will appear as shown in Figure 3.113.

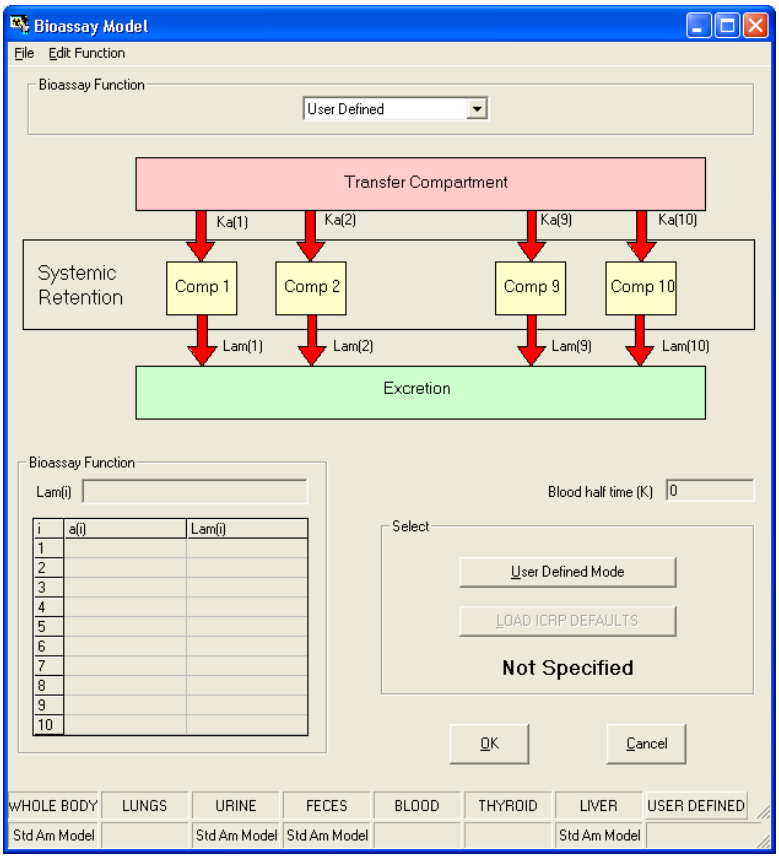


Figure 3.113. The **Bioassay Model** window confirming that ALL **ICRP-default** parameters have been loaded.

Note that the *indicators* on the bottom row of the **Bioassay Model** window record that the "**Std Am Model**" (in this example) has been loaded. These *indicators* specify the **WHOLE BODY**, **URINE** and **FECES**, which are the only "*standard*" *Bioassay Quantities* used for americium. *Clicking* "**OK**" closes this window - and returns you to the **Main Screen**.

The **Status Bar** (Figure 3.114) records that the following **ICRP-default** parameter values have been loaded (by your *click* of the "**ICRP DEFS Load**" *button*):

- **Absorption Type** - "**M**" was selected;
- **Particle Transport**;
- **GI-Tract**;
- f_1 - "**0.0005**" was selected along with the **Type M** absorption;
- **Biokinetics** - "**Am**" was selected (the **Indicator Nuclide**);
- **Deposition** - the **respiratory tract** model;
- **AMAD** - "**5**" µm.

The "**Wound**" model was NOT specified. This is NOT an "***ICRP default***."

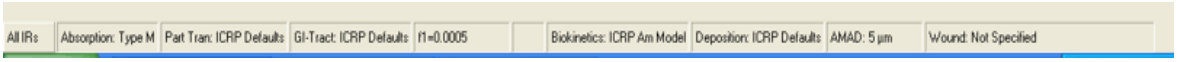


Figure 3.114. The Status Bar indicating that ALL **ICRP-Default** parameter values have been loaded (for **Type M americium**).

Note: Using the "**ICRP DEFS Load**" tool also loads ICRP-default parameter values for **Dose Calculation**, *i.e.*, the *ICRP Publication 60/68* radiation weighting factors, tissue weighting factors, and remainder tissue rules (see **Appendix A: Technical Basis**, Section A.3. - "**Radiation and Tissue Weighting Factors**").

3.8.10.2. 10-CFR-835 Prescribed Parameters

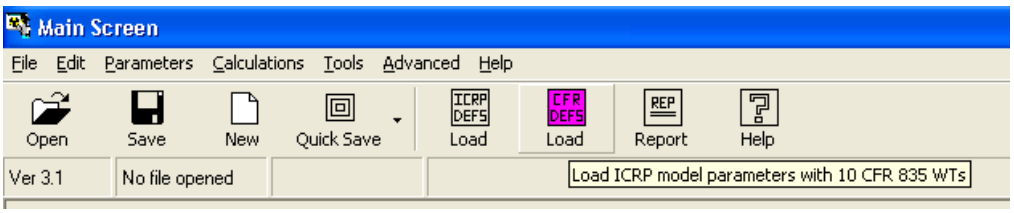


Figure 3.115. The "**CFR DEFS Load**" *tool button*.

If you ***move*** your *mouse pointer* over the "**CFR DEFS Load**" *button* in the **Tool Bar**, the "**CFR DEFS**" symbol will change color - to *purple* (Figure 3.115). *Clicking* the *button* will then display the "**F1 values**" window (as shown in Figure 3.112, above) - from which you can again *select* the **row** with your required combination of ***ICRP-DEFAULT* Absorption Type** and f_1 value. When you then *click* "**OK**", IMBA Expert™ OCAS/ORAU-Edition will *load* ALL of the ***ICRP-DEFAULT* Biokinetic Model** AND **Bioassay Model** parameters. ***However***, the loaded radiation weighting factors **(w_R)**, tissue weighting factors **(w_T)**, and remainder tissue rules will be those prescribed by the 10-CFR-835 Regulation.

3.8.11. Setting Up Different Model Parameters for Each IR

By **default**, IMBA Expert™ OCAS/ORAU-Edition stores and applies a **single set of parameter values** for each **Model**, *i.e.*, the last-loaded set of parameter values for those of the following models that you have defined:

1. **Deposition** model;
2. **Particle Transport** model;
3. **Absorption** model;
4. **Wound** model;
5. **GI-Tract** model;
6. **Biokinetic** models;
7. **Bioassay** models.

In IMBA Expert™ OCAS/ORAU-Edition, you can define up to **10 Intake Regimes** (**IRs**), each of which can be selected from **Inhalation**, **Ingestion**, **Injection** (or, in future, **Wound**). Calculations for each of these four different **Routes** of intake use a different combination of **Models**, as follows (by **Model #**):

- **Inhalation** - model ## 1, 2, 3, 5, 6 and 7;
- **Ingestion** - model ## 5, 6 and 7;
- **Injection** - model ## 6 and 7;
- **Wound** - model ## 4, 6 and 7.

Therefore, in the *default* mode where each of the seven types of model can have only ONE defined set of parameters, the **Model Parameters** sub-panel and **Status Bar** are displayed as shown in Figure 3.116.

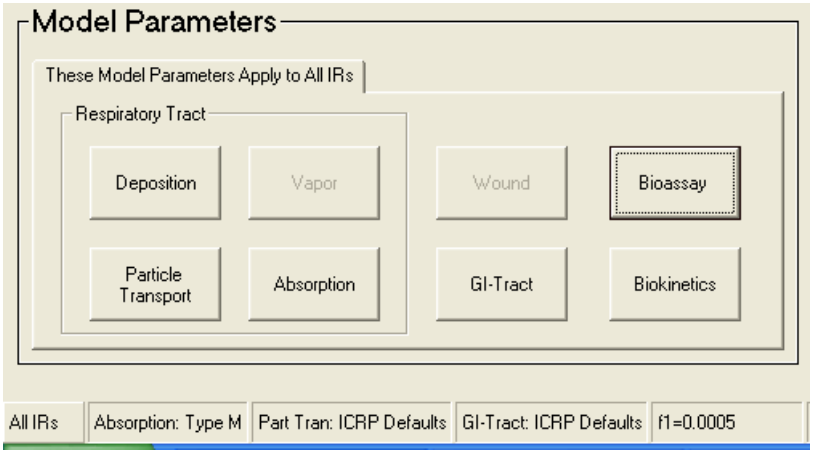


Figure 3.116. The **Model Parameters** sub-panel and **Status Bar** in the "**These Model Parameters Apply to All IRs**" mode.

In this *default* mode, if several of the **IRs** are by **Inhalation**, then for example you can define only a single set of **Aerosol Parameters** (**Ventilation Rate**, **AMAD**, σ_g, **ρ** and **SF** - in **model #1**), or **Absorption Parameters** (**Absorption Type** and f_1 value - in **model #3**). This would limit you to analyzing simultaneously multiple intakes of only the same type of material (with the same aerosol characteristics).

IMBA Expert™ OCAS/ORAU-Edition overcomes this limitation by enabling you to define *independently* ALL model parameters for **each IR**. To do this, you first *de-select* (*un-tick*) the "**Apply Model Params to All IRs**" *option* in the **Advanced** menu (Figure 3.117).

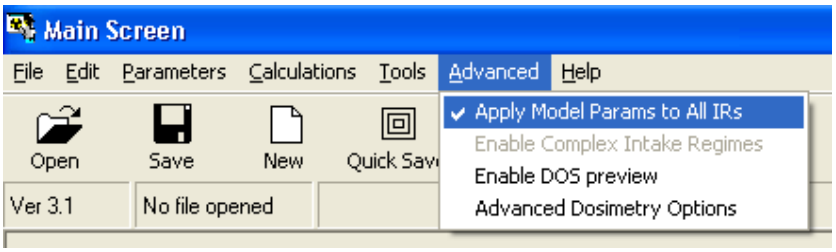


Figure 3.117. De-selecting "**Apply Model Params to ALL IRs**" in **Advance**d menu.

The **Model Parameters** sub-panel will then change to display multiple **Index Tabs** - one for *each* **IR**. You can then set up specific parameter values for each individual **IR #**. *Click* on the **IR #** *tab index* - to display all of its associated model *options* (Figure 3.118). The parameter values for every model specified in the **Model Parameters** sub-panel will now be applied ONLY for the *indexed* **IR #** (*i.e.*, **IR# 5** in the example shown in Figure 3.118).

Note: In this "*independent models*" mode, the **Index Tabs** in the **Intake Regimes** and **Model Parameters** sub-panels are linked. You can change the displayed **IR #**, and its associated set of **Models**, by *clicking* a new **IR # Tab** in *either* sub-panel.

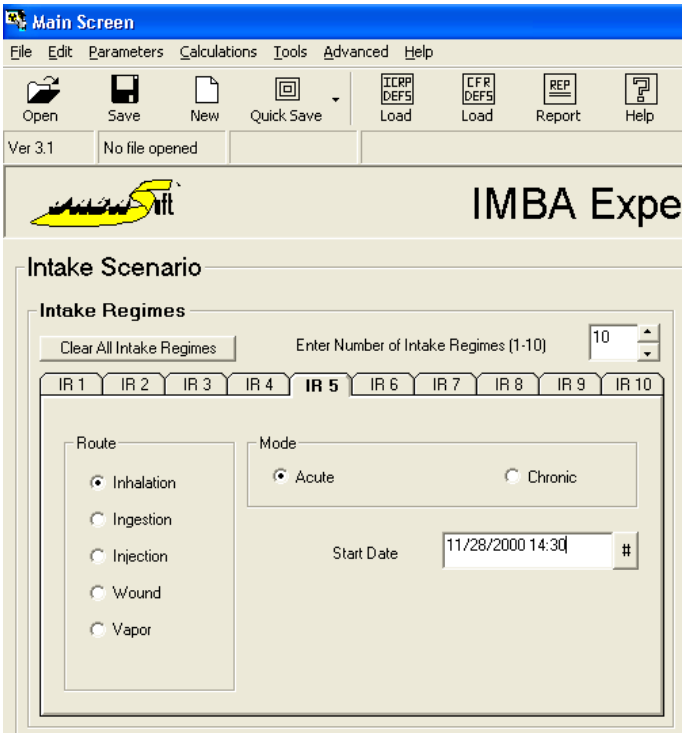


Figure 3.118. Display mode for setting up model parameters *independently* for each **IR**.

Key Tip: This *multi-dimensional-model* capability is useful not just for analyzing several known intake events (of *different* materials). It can also be used to "*fit*" an *unknown* value of a critical parameter for a single intake, *e.g.*, the aerosol AMAD or solubility type. IMBA Expert™ OCAS/ORAU-Edition can be set up for several simultaneous instances of the same intake event, assuming various hypothetical parameter values for each instance. IMBA Expert™ OCAS/ORAU-Edition can then automatically determine which set of parameter values is most likely, based on the bioassay data.

3.8.12. Saving All Model Parameters

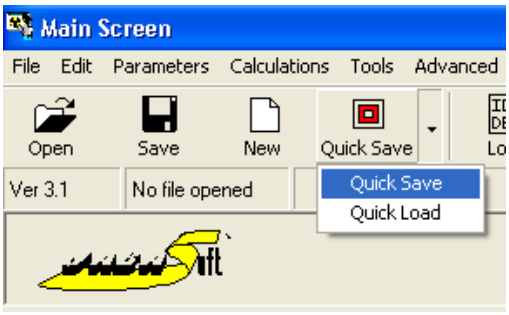


Figure 3.119. The "***Quick Save***" *tool button* for **Saving All Model Parameters** (and calculated results).

At any time while you are using IMBA Expert™ OCAS/ORAU-Edition to set up (or change) parameter values or model options, you can **Save** a complete record of the current status

(including all selected model options and parameter values, together with the most recently calculated results). You can do this in any of the following ways.

3.8.12.1. Using the "Quick Save" Tool Button

Clicking the "**Quick Save**" *tool button* (Figure 3.119) saves all parameter values and results to the default **Parameter File** named "**parameters.ix**." This is located in the folder "**[Install Drive:]\JABASOFT\IMBAEXUS**," where **[Install Drive:]** is the disk drive (root directory) on which you installed IMBA Expert™ OCAS/ORAU-Edition. If you accepted the default installation option, this will be **[C:]**.

Warning: "**Quick Save**" will over-write any existing "**parameters.ix**" file - so this facility should be used only as a **temporary file**, *e.g.*, to save your work periodically as you proceed through setting up a complex case study.

Note: The "**Quick Save**" *tool button* only appears on the **Main Screen**. However, you can return to the **Main Screen** from either of the **Calculations** screens - at any time except when IMBA Expert™ OCAS/ORAU-Edition is performing a calculation.

3.8.12.2. Using the "Save" Option

Clicking the "**Save**" *tool button* (Figure 3.119) saves all parameter values and results to the **Parameter File** named (with its location) in the parameter file box. However, if you are working with a "**New**" (and un-named) parameter file, then you will be prompted for the **File name** for your saved parameter file (Figure 3.120). The default location in which your file will be saved is **[Install Drive:]\JABASOFT\IMBAEXUS\UserData1**. You can **browse** to save the file in any other folder.

Warning: IMBA Expert™ OCAS/ORAU-Edition will automatically enter the last-used parameter file name (for the current session) in the "**Save As**" dialog box. If you do NOT want to over-write that file, be sure to change the file name BEFORE *clicking* ***Save***.

Note: *Selecting* **"File | Save"** from the **Menu Bar** performs exactly the same function as the "**Save**" *tool button*.

Note: The "**Save**" *tool button* also appears on the **Bioassay Calculations** and **Dose Calculations** screens. The **File | Save** *menu option* is available in both the **Main Screen** and **Dose Calculations Screen**.

3.8.12.3. Using the "File | Save As" Option

The "**Save As**" window, and "**File name**" *dialog box* (Figure 3.120) always appear when you select "**File | Save As**" from the **Menu Bar** (in the **Main Screen**).

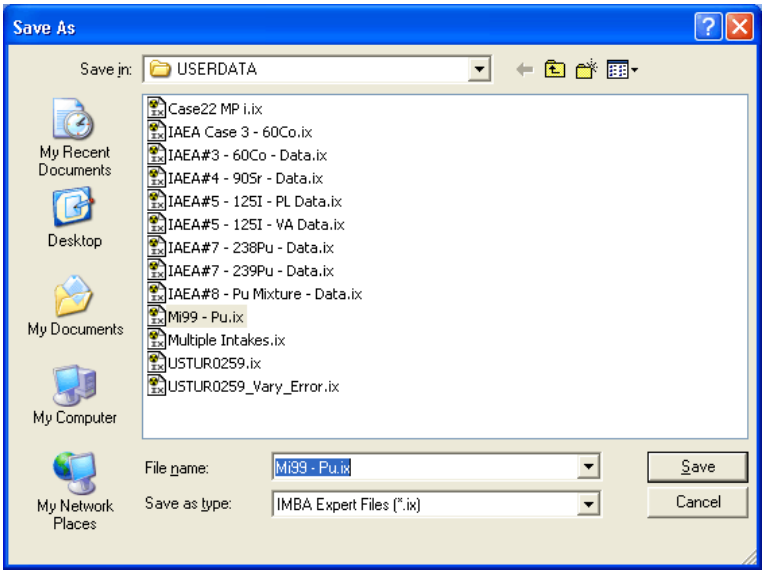


Figure 3.120. The "**Save As**" dialog box opened automatically by the "**Save**" *tool button* when no **Parameter File** name has been specified.

3.8.13. Example Parameter File

The parameter file named "**Mi99 - Associated Nuclides.ix**" that was put in your **[Install Drv]:\JABASOFT\IMBAEXUS\UserData\Demo** folder when you installed IMBA Expert™ OCAS/ORAU-Edition. This is an example (partly hypothetical) of a case that involves:

- the **Indicator Nuclide** ^{239}**Pu**;
- two **Associated Radionuclides** (^{239}**Pu** and ^{241}**Am**);
- three **Intake Regimes**.

To *view* the content of this file (or any "***.ix**" file), go to your **UserData\Demo** folder and *right-click* on the file. *Choose* to *open* the file in the text file editor **MS Notepad**.

Note: All "***.ix**" files are of standard structure (and **VERY long**). They contain **ALL** the information entered about this case - plus the calculated results. In "**Mi99 - Pu.ix**" many of the saved values are **ZERO** or **"*"**. These represent "**null**" values, *e.g.*, non-defined values for the remaining **seven** available **Intake Regimes** (**IR4 - IR10**) not used in this case.

3.9. Calculations Sub-panel

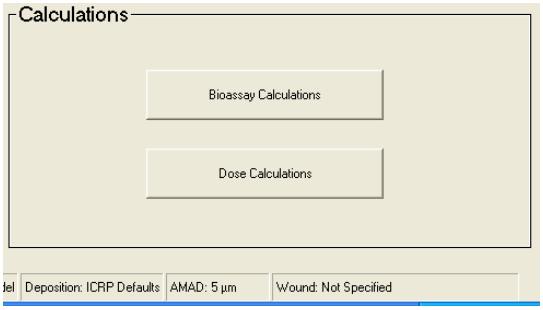


Figure 3.121. The **Calculations** Sub-panel.

This sub-panel provides the only *portal* between the **Main Screen** and the two "**Calculations**" screens:

- **Bioassay Calculations** - *click* this *button* to open the ***Bioassay Calculations*** screen (set up the **bioassay calculations**, estimate the amount(s) of **Intake(s)**, and/or predict **Bioassay Quantities**);

- **Dose Calculations** - *click* this *button* to open the ***Dose Calculations*** screen (set up the **dose calculations** and calculate **Doses**).

4. How to Use the Bioassay Calculations Screen

The **Bioassay Calculations** screen (Figure 4.1) opens when you click the "**Bioassay Calculations**" button (on the **Main Screen**).

The screen works as follows:

1. You *select* the direction of the CALCULATION in the center of the screen. This can be *from* BIOASSAY QUANTITY *to* INTAKE(S) - the default setting, or *from* INTAKE(S) *to* BIOASSAY QUANTITY.

2. The **calculated** (or **hypothetical**) values of INTAKE(S) are displayed on the left.

3. The **predicted** and/or **measured** values of the BIOASSAY QUANTITY are displayed on the right.

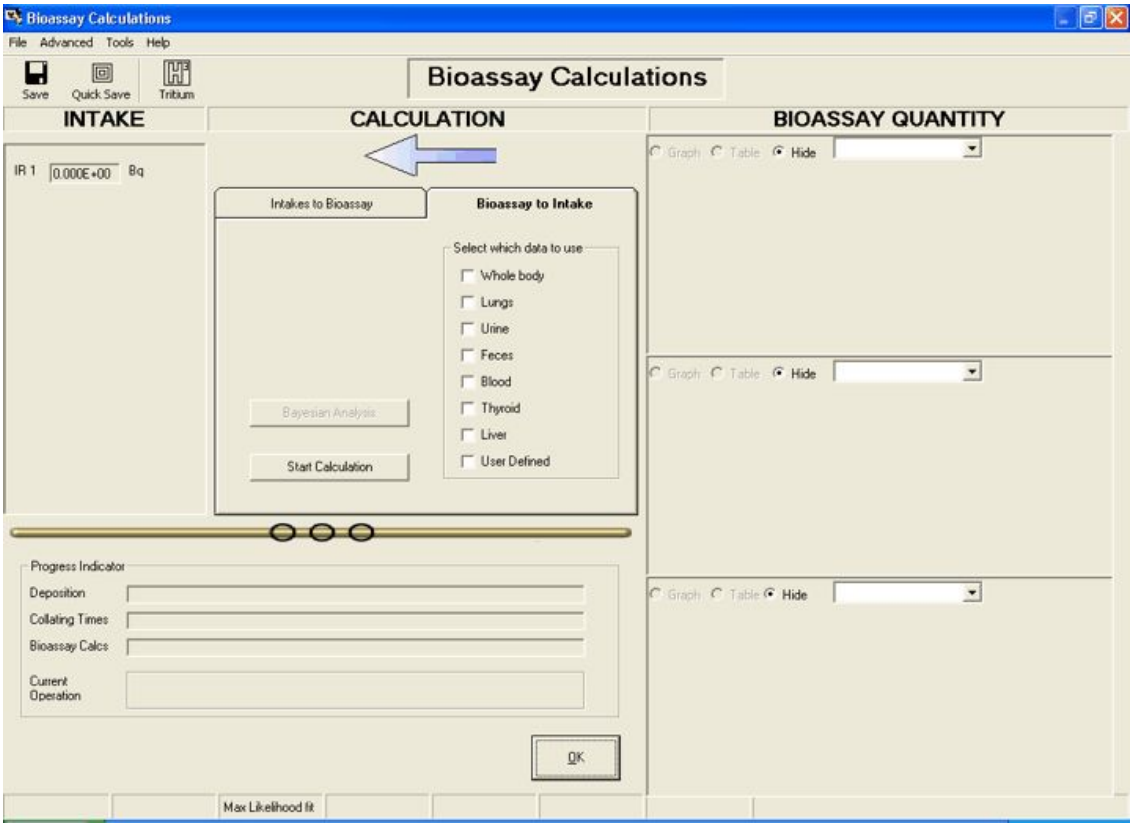


Figure 4.1. The **Bioassay Calculations** screen.

The **Bioassay Calculations** screen is divided into these functional parts - from the top:

- **Menu Bar**.
- **Short-cut Icons**.

Main panel:

1. **Intake Sub-panel** - left side
2. **Calculation Sub-panel** - center
3. **Bioassay Quantity Sub-panel** - right side - used to *enter* and *display* **bioassay data**.

Bottom left corner panel:

- **Progress Indicator**.

4.1. Bioassay Menus

The **Menu Bar**, shown at the top of the **Bioassay Calculations** window, gives the following options:

- **File** menu.
- **Advanced** menu.
- **Tools** menu.
- **Help** menu.

4.1.1. Bioassay File Menu

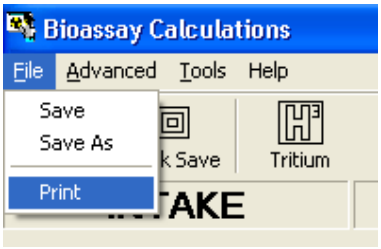


Figure 4.2. Drop-down bioassay **File** list box.

Click **File | Print** to send a screen dump of the displayed **Bioassay Calculations** screen to your Windows® printer - *e.g.* Figure 4.3.

Figure 4.3 shows the printed image of the **Bioassay Calculations** screen with the example parameter file "**USTUR0259.ix**" loaded.

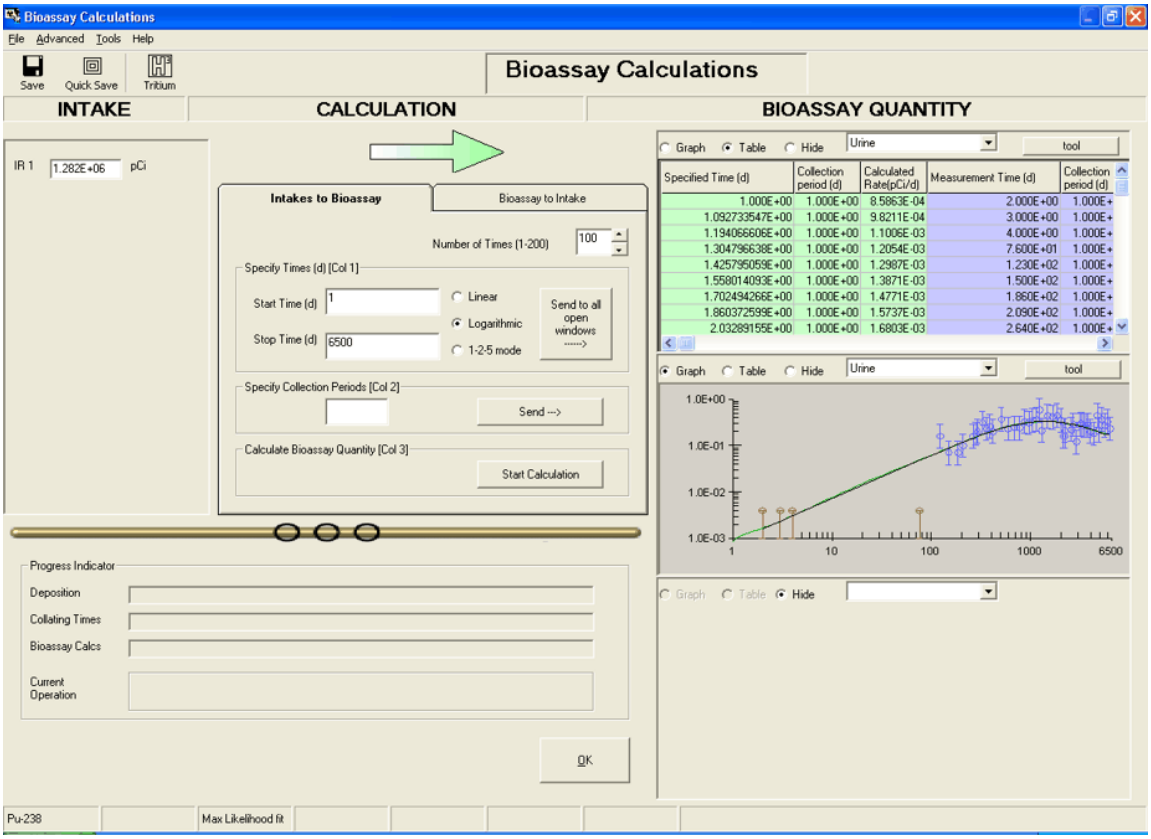


Figure 4.3. Printed screen dump of **Bioassay Calculations** screen.

4.1.2. Bioassay Advanced Menu

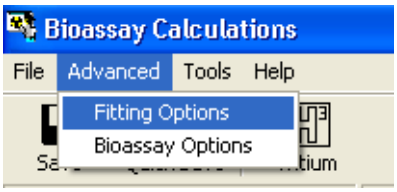


Figure 4.4. Advanced menu options for **Bioassay Calculations**.

The "**Advanced**" menu enables you to select from the following **Advanced Dosimetry Options**:

- **Fitting** - *select* from "**Least Squares**", "**Maximum Likelihood**" (the default), or "**Bayesian**" fitting methods (Figure 4.5).
- **Bioassay** - *enable* (Figure 4.6) the *special feature* to calculate **in-growth of Am-241 activity** *in the lungs* from an intake of plutonium isotopes (containing a known fraction of ^{241}**Pu** activity).

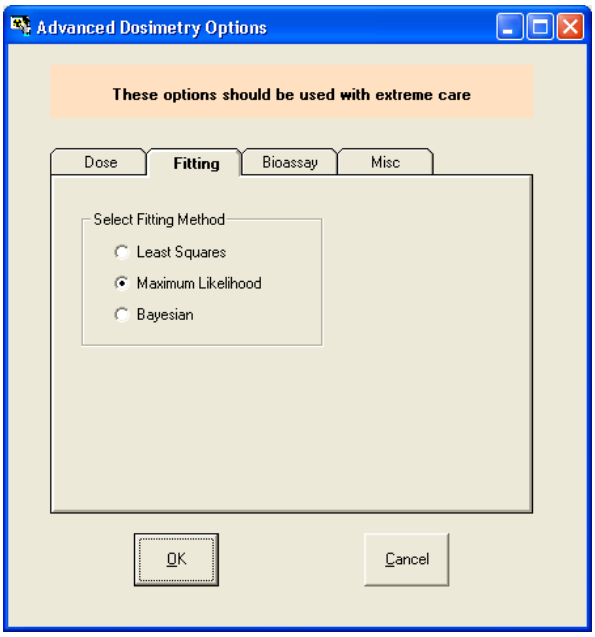


Figure 4.5. Selecting **Fitting** options in the **Advanced Dosimetry Options** window.

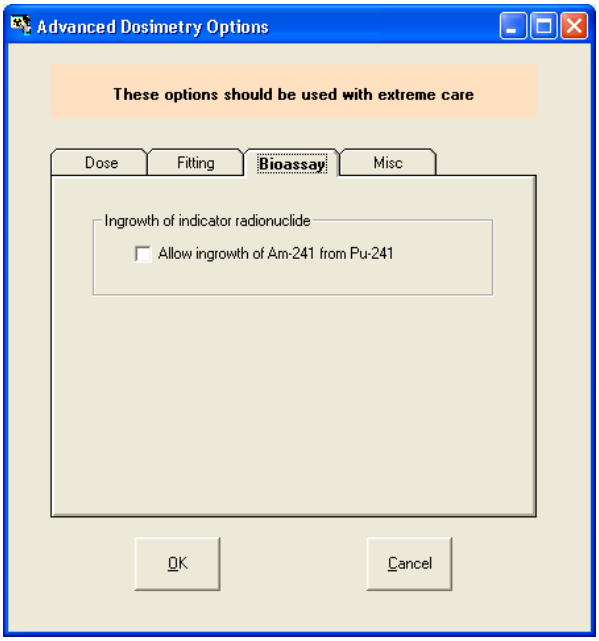


Figure 4.6. Enabling the **Bioassay** option to measure in-growth of ^{241}**Am** activity (from ^{241}Pu).

4.1.3. Bioassay Tools Menu

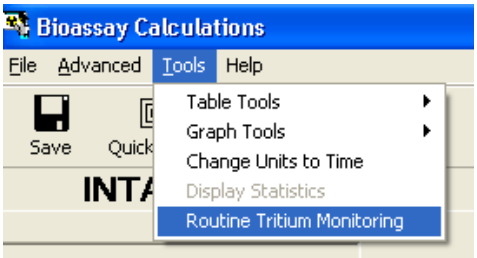


Figure 4.7. Drop-down **Bioassay Tools** list box.

The Bioassay Tools options are:

- **Table Tools** - Enable you to *open* the **Table Tool** (spreadsheet-like facility) to *enter* and/or *edit* bioassay data, sample time (or date), and sample duration (for urine and feces), for any **one** of the three **Bioassay Quantity** windows (see Figure 4.8).

- **Graph Tools** - Enable you to *open* the **Graph Tool** (graph editing facility) to *specify* how you want a graph to be displayed (ranges of the x- and y-axes, linear or logarithmic plots) for any **one** of the three **Bioassay Quantity** windows (see Figure 4.9).

- **Change Units to Time/Date** - *toggle* instantly between **Time Units** of **Date** or **Time (d)** throughout the program (all three screens) - see Figures 4.10 - 4.12.

- **Routine Tritium Monitoring** - *open* a special tool for direct analysis of routine tritium bioassay results.

4.1.3.1. Table Tools

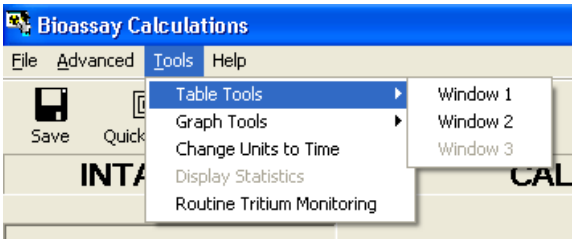


Figure 4.8. Drop-down list of **Bioassay Quantity** windows for using **Table Tools**.

4.1.3.2. Graph Tools

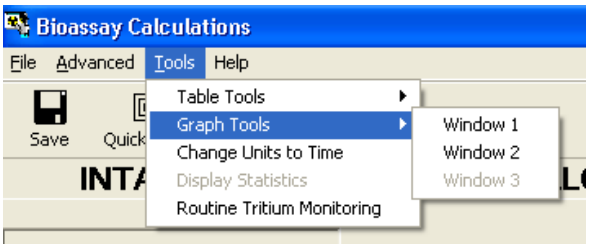


Figure 4.9. Drop-down list of **Bioassay Quantity** windows for using **Graph Tools**.

4.1.3.3. Toggle Time/Date

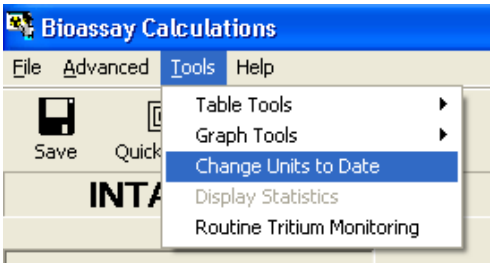


Figure 4.10. Toggle control to change the **Time Units**.

Selecting "**Change Units to Date**" will switch the **Time Unit** shown in all **Bioassay Quantity** tables to **Date (+hh:mm)** - calendar **Date** plus two-digit **Hour** and **Minute** values (Figure 4.11).

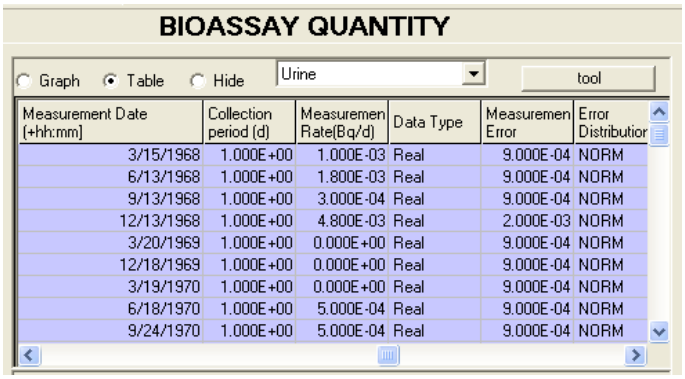


Figure 4.11. Displaying when samples were taken as a **Date (+hh:mm)** as the alternative to the default display of **Time (d)**.

The label of the **Change Time Units** control will switch automatically once you make a change (Figure 4.12) - so that you can easily *toggle* back to the original **Time/Date** unit.

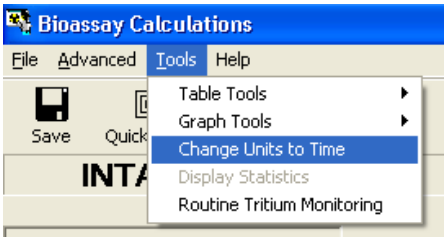


Figure 4.12. "**Change Units**" label switches automatically to enable toggling between **Time** and **Date**.

4.1.3.4. Routine Tritium Monitoring

Selecting "**Routine Tritium Monitoring**" from the "**Tools**" menu opens the "**Tritium Routine Monitoring Tool**" window (Figure 4.13). This is a special tool to simplify the process of calculating effective dose based directly on a series of routine tritium urinalyses. Use of this tool is illustrated in **Appendix D: Example Bioassay Cases – "Case of Routine Tritium Urinalysis"**. This tool is being further developed (by NRPB) as part of the European IDEAS project (Doerfel et al 2003).

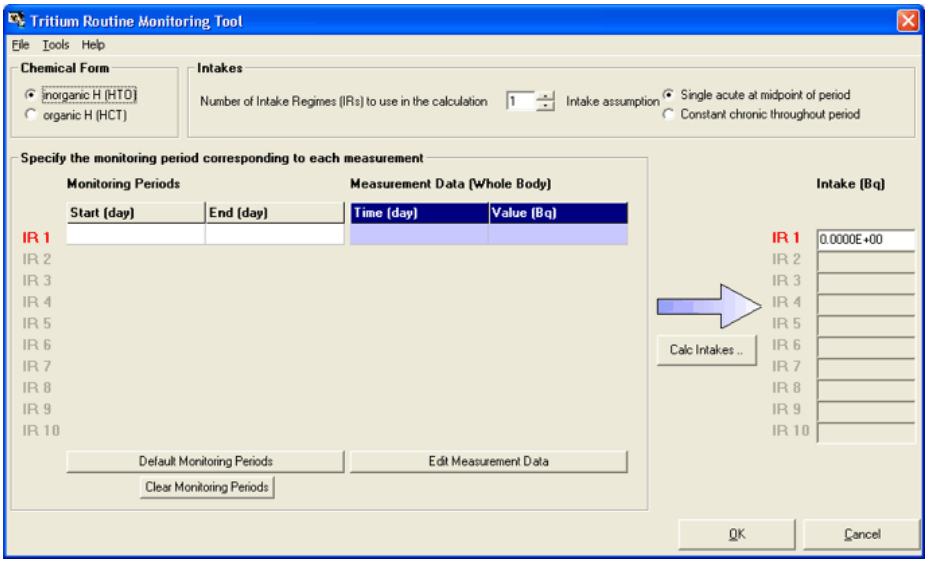


Figure 4.13. Calculator Tool for **routine tritium urinalysis**.

4.1.4. Bioassay Help Menu

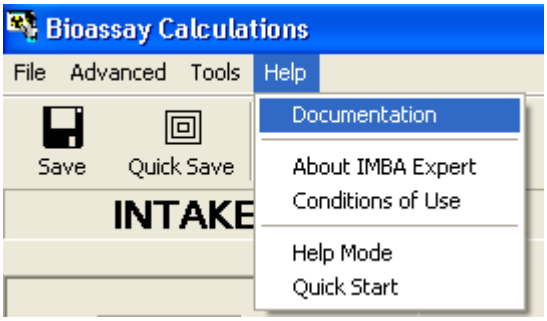


Figure 4.14. Drop-down **Bioassay Help** list box.

The **Help** features available from the **Help Menu** in the **Bioassay Calculations** screen are the same as those available from the **Main Screen** (Figures 3.16 through 3.20) - except for the link to "**Check for Updates**". So, while setting up **Bioassay Calculations**, you do NOT have to return to the **Main Screen** to access the primary **Help** features.

4.2. Data Housekeeping

The **Bioassay Calculations** screen is designed to:

1. Make it easy for you to Save your entered data at any stage of data entry.

2. Make it easy for you to use a "Short-Cut" analysis technique for **routine tritium bioassay**.

3. Make it easy for you to Exit and return to the **Main Screen** (to revise **Model Parameters** and/or **Intake Regimes**) without losing any of your bioassay data.

4.2.1. Bioassay Save Icons

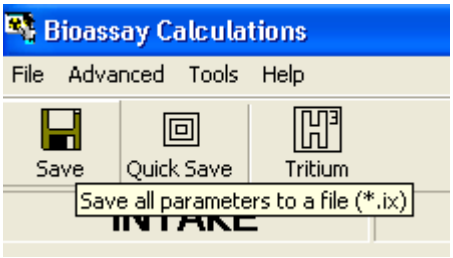


Figure 4.15. Bioassay Save icon.

Clicking the "**Save**" icon in the **Bioassay Calculations** screen saves all of the displayed values in the current **Parameter File** ("***.ix**"). You can do this at any time (except when IMBA Expert™ OCAS/ORAU-Edition is performing a calculation), for example, at several points while entering a long series of bioassay data. When you *exit* the **Bioassay Calculations** screen (to return to the **Main Screen**), the **Parameter File** is automatically updated with all of the displayed data.

Clicking the "**Quick Save**" icon (Figure 4.16) saves all of the displayed values (and all other parameter values) in the default **Parameter File** (named "**Parameters.ix**").

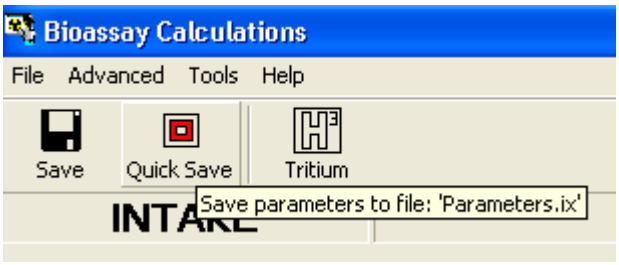


Figure 4.16. Bioassay Quick Save icon.

4.2.2. Routine Tritium Monitoring Icon

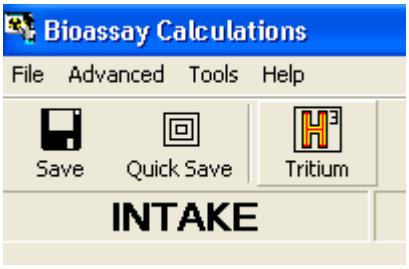


Figure 4.17. Tritium icon.

Clicking the "**Tritium**" icon (Figure 4.16) in the **Bioassay Calculations** screen opens the "**Tritium Routine Monitoring Tool**" window (shown above as Figure 4.13). This provides a "short-cut" method for calculating the total amount of tritium intake over a series of routine urinalysis monitoring periods (and the resulting effective dose), without having to identify individual intake events manually from the bioassay data. For a worked example of how to use this screen see **Appendix D: Example Bioassay Cases:** "**Case of Routine Tritium Urinalysis**".

4.2.3. Closing the Bioassay Calculations Screen

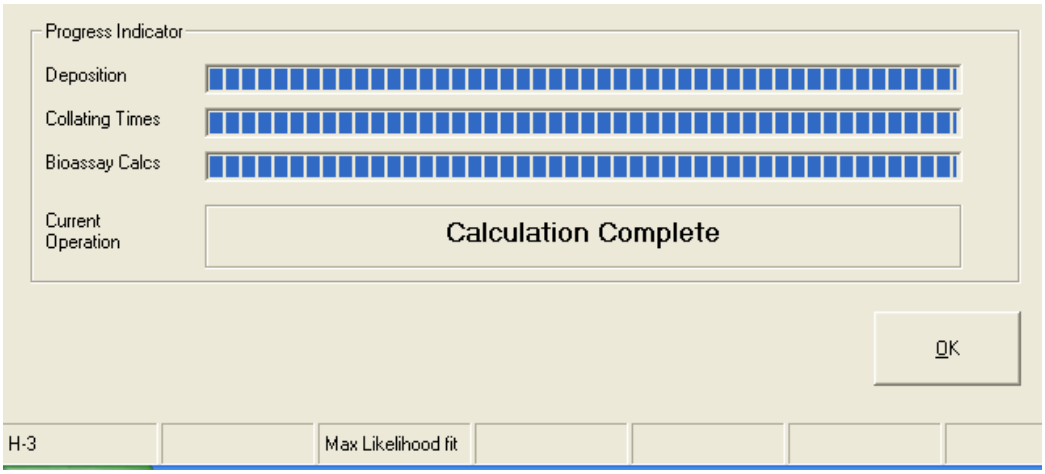


Figure 4.18. The "**OK**" *button* for closing and exiting the **Bioassay Calculations** screen.

You can return to the **Main Screen** at any time (except when IMBA Expert™ OCAS/ORAU-Edition is performing a bioassay calculation) by *clicking* the "**OK**" *button* (bottom-left panel of the **Bioassay Calculations** screen - see Figure 4.18).

	Warning: Using the "**OK**" *button* to *close* the **Bioassay Calculations** screen leaves all of the values that were displayed (and the current values of non-displayed bioassay data) in **memory**. It does NOT automatically *save* these values to the **Parameter File**. You must choose to do this yourself - by *clicking* the "**Save**" icon. If you *exit* IMBA Expert™ OCAS/ORAU-Edition without first *saving* the **Parameter File**, any updated parameter values will be **lost**.
	Tip: You can also *exit* the **Bioassay Calculations** screen by *clicking* the Windows® "**X**" in the top-right corner of the screen. Again, this leaves the bioassay data in **memory**, but NOT *saved* to the **Parameter File**.

4.3. Performing Bioassay Calculations

All bioassay calculations are *run* from the **CALCULATION** panel - top-center of the **Bioassay Calculations** screen. The calculation can go in either direction:

1. From **right** to **left** - Bioassay Quantity (Measurements) to estimated Intake(s) - as indicated by a **blue** arrow (Figure 4.19).

2. From **left** to **right** - value(s) of Intake(s) to predicted Bioassay Quantity - as indicated by a **green** arrow (Figure 4.20).

The **arrow** color indicates whether the bioassay data shown in a **Bioassay Quantity Table** are **measured** or **predicted** values, *i.e.*:

1. **Measured** bioassay values are always displayed on a **blue** background.

2. **Predicted** bioassay values are always displayed on a **green** background.

The same **color coding** is used for a **Bioassay Quantity Graph**, *i.e.*:

1. **Blue** lines are used to join the values of a **Bioassay Quantity** that are **fitted** to the **measured** data.

2. **Green** lines join the **predicted** values of a **Bioassay Quantity**.

You can *toggle* the bioassay calculation in either direction, simply by *clicking* the **colored arrow** (to reverse its direction) - or by *selecting* the required **index tab** ("**Intakes to Bioassay**" or "**Bioassay to Intake**").

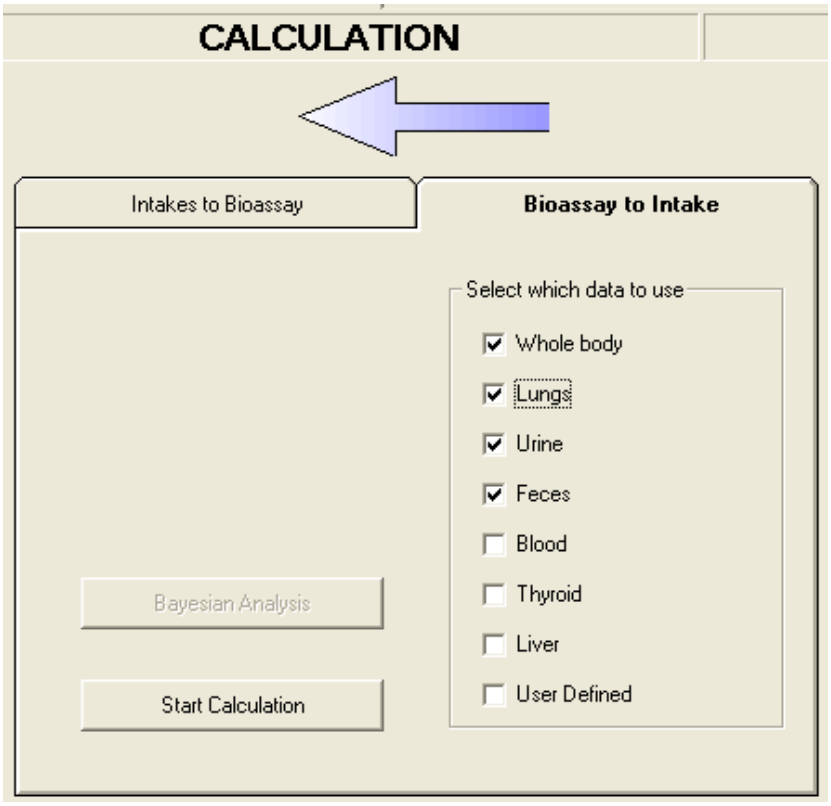


Figure 4.19. Bioassay calculation set as "**Bioassay to Intake**" and indicated by a **blue** arrow.

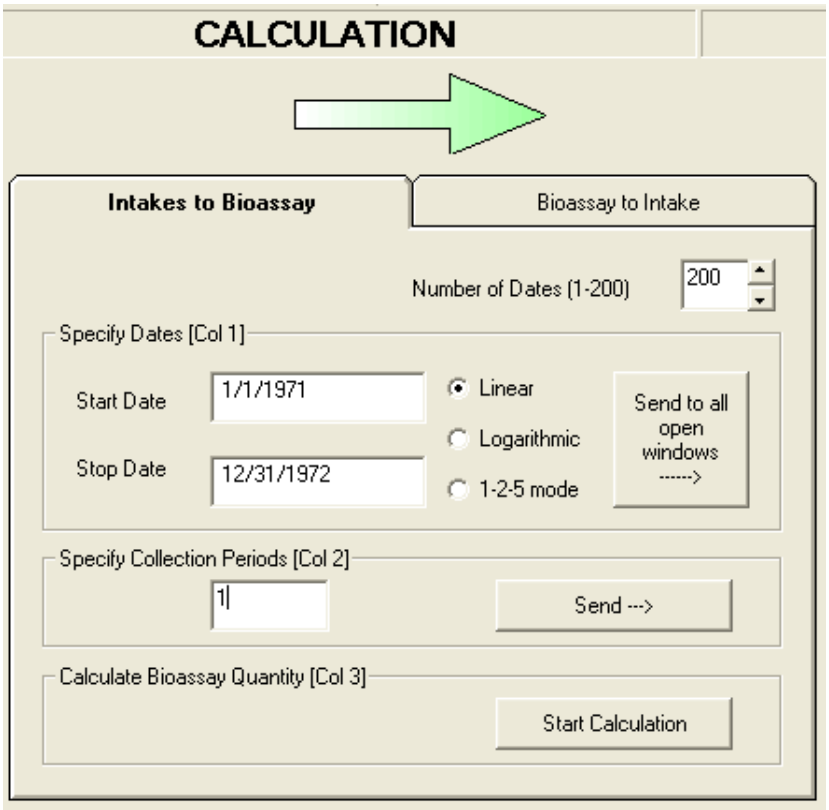


Figure 4.20. Bioassay calculation set as "**Intakes to Bioassay**" and indicated by a **green** arrow.

4.3.1. From Bioassay Measurements to Intake(s)

For a single intake (and a single set of bioassay data), provided that the time of the intake and the aerosol and absorption characteristics of the material are known, then calculation of the most likely amount of intake is simple and straightforward.

However, for multiple intakes without precise knowledge of the times and nature of the intakes, estimating the intake amounts must be done by **iteration**. In general, this will involve:

- *Defining* a hypothetical set of parameter values to provide an **initial estimate** of the intake amounts.
- *Examining* the "goodness-of-fit" of the corresponding predicted bioassay quantity to the measured bioassay data.
- *Refining* the assumed values of unknown parameters (within realistic bounds).
- *Calculating* the resulting new estimates of the intake amounts.
- *Re-examining* the resulting "goodness-of-fit" of the predicted bioassay quantity.
- *Repeating* this iterative process until an adequate fit to the measured bioassay data is obtained (with justifiable parameter values).

IMBA Expert™ OCAS/ORAU-Edition provides the computational tools needed to facilitate the iterative "fitting" process, while allowing you to control this by exercising your own judgment. You can switch very easily between estimating the intake amounts and graphically comparing the predicted and measured values, as you proceed through the iterative process of refining the assumed parameter values.

Appendix D: Example Bioassay Cases gives **step-by-step** examples (with real data) of:

1. estimating a **single intake** at a known time and for known material characteristics;
2. estimating **three separate intakes** with uncertain times of intake and material characteristics.
3. estimating an intake using **multiple bioassay quantities**.

These elementary examples will introduce you to the main "**built-in**" features and functions of IMBA Expert™ OCAS/ORAU-Edition that are provided for **bioassay analysis**. Or, you can "**browse**" through the **Visual Tour** of all features and functions available for bioassay calculations.

- **Example** of simple estimation of single intake – **Appendix D, Section D.2.**
- **Example** of iterative estimation of multiple intakes – **Appendix D, Section D.3.**
- **Example** of estimating intake using multiple bioassay quantities – **Appendix D, Section D.4.**
- **Visual Tour** of the **Bioassay Calculations** screen and its functions – given earlier **(Section 2.2.)**.

4.3.2. From Intake(s) to Bioassay Quantity

Calculation of the amount of a **Bioassay Quantity** as a function of the **Time** variable is used to:

- plan a **Bioassay Program** - by calculating the **expected amount** at prescribed **time points**;
- provide **fine time-resolution** in the **predicted bioassay quantity** for graphical comparison with the measured data - as an integral part of the **fitting procedure for estimating Intake(s)**.

The application of the "**Intakes to Bioassay**" calculation to the **fitting procedure** is illustrated in Figure 4.16. See also:

- **“Example of a Single Intake Estimation” – Appendix D, Section D.2.**
- **“Example of a Multiple (Iterative) Intake Estimation” – Appendix D, Section D.3.**
- **“Example of Multiple Bioassay Quantities” – Appendix D, Section D.4.**

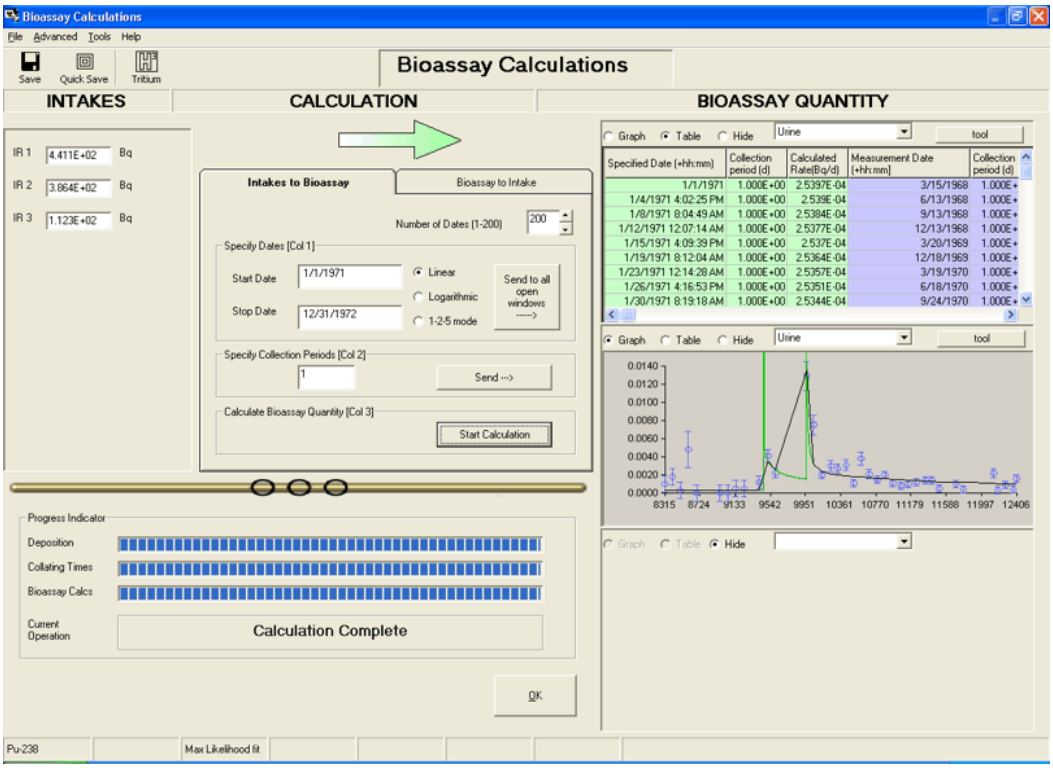


Figure 4.21. "**INTAKES**" sub-panel displays **Intake** amounts for up to ***10*** **Intake Regimes** (**IRs**).

4.4. ^{241}Am Activity in Lung As an Indicator of ^{241}Pu Intake

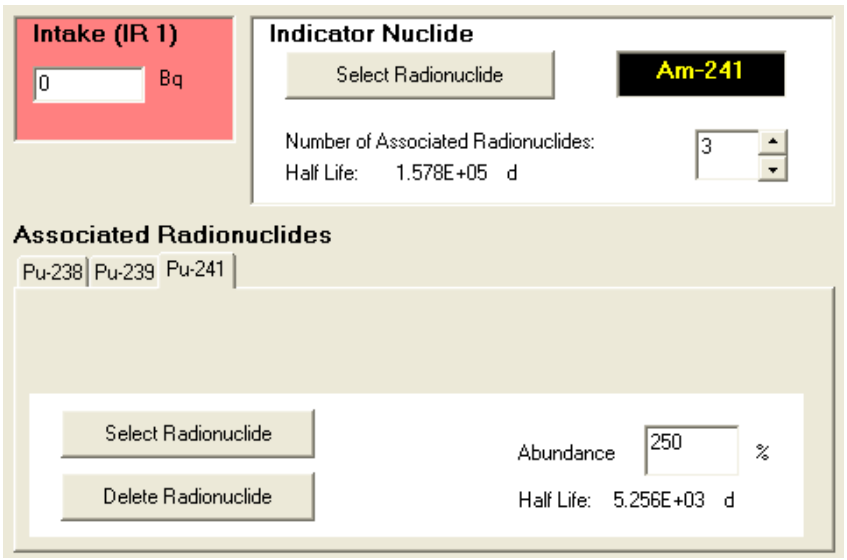


Figure 4.22. Combination of ^{241}**Am** as the *Indicator Nuclide* and ^{241}**Pu** as an *Associated Radionuclide*.

In cases where inhalation of relatively insoluble forms of plutonium has occurred, and the inhaled plutonium contains a significant amount of ^{241}**Pu**, higher sensitivity for lung counting can often be achieved by measuring the activity of the ^{241}**Am** progeny (59.5 keV and 35.7% abundance **γ-ray**) rather than the low-energy and low-abundance **L X-rays** emitted by ^{239}**Pu** (and ^{238}**Pu**). For particulate material retained in the respiratory tract, it is reasonable to assume that the absorption of ^{241}**Am (**from the particle matrix) will occur at the same rate(s) as that of the plutonium isotopes. Thus, the ^{241}**Am** activity measured in the lungs should be a good indicator of the parent ^{241}**Pu** activity, and thus the total retained plutonium activity. However, account must be taken of the 14-y decay half-life of ^{241}**Pu**, and the subsequent in-growth of the ^{241}**Am** activity. IMBA Expert™ OCAS/ORAU-Edition includes a special tool to enable this decay and in-growth to be accounted for automatically. Thus, measurements of ^{241}**Am** activity in the lungs can be used to calculate the total lung retention of a defined mixture of plutonium isotopes.

In order to activate this special tool, it is first necessary to define ^{241}**Am** as the *Indicator Nuclide* and ^{241}**Pu** as an *Associated Radionuclide* (Figure 4.22). The tool can be activated (Figure 4.23) from EITHER the *Main Screen* ("**Advanced | Advanced Dosimetry Options**" menu) OR the *Bioassay Calculations Screen* ("**Advanced | Bioassay Options**" menu).

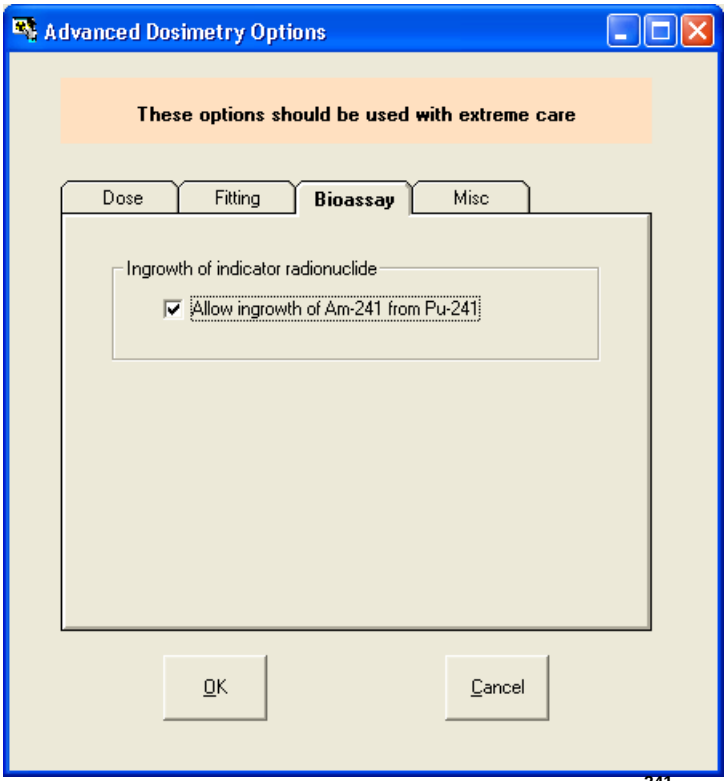


Figure 4.23. Bioassay option to track "in-growth" of ^{241}**Am** as the *Indicator Nuclide* for ^{241}**Pu** in the lungs.

For a worked example of how to use this "^{241}**Am in-growth**" tool, see **Appendix D: Example Bioassay Cases: "Case of Am-241 Lung Counting (for Pu-241)"**.

4.5. Using the Table Tool for Data Entry

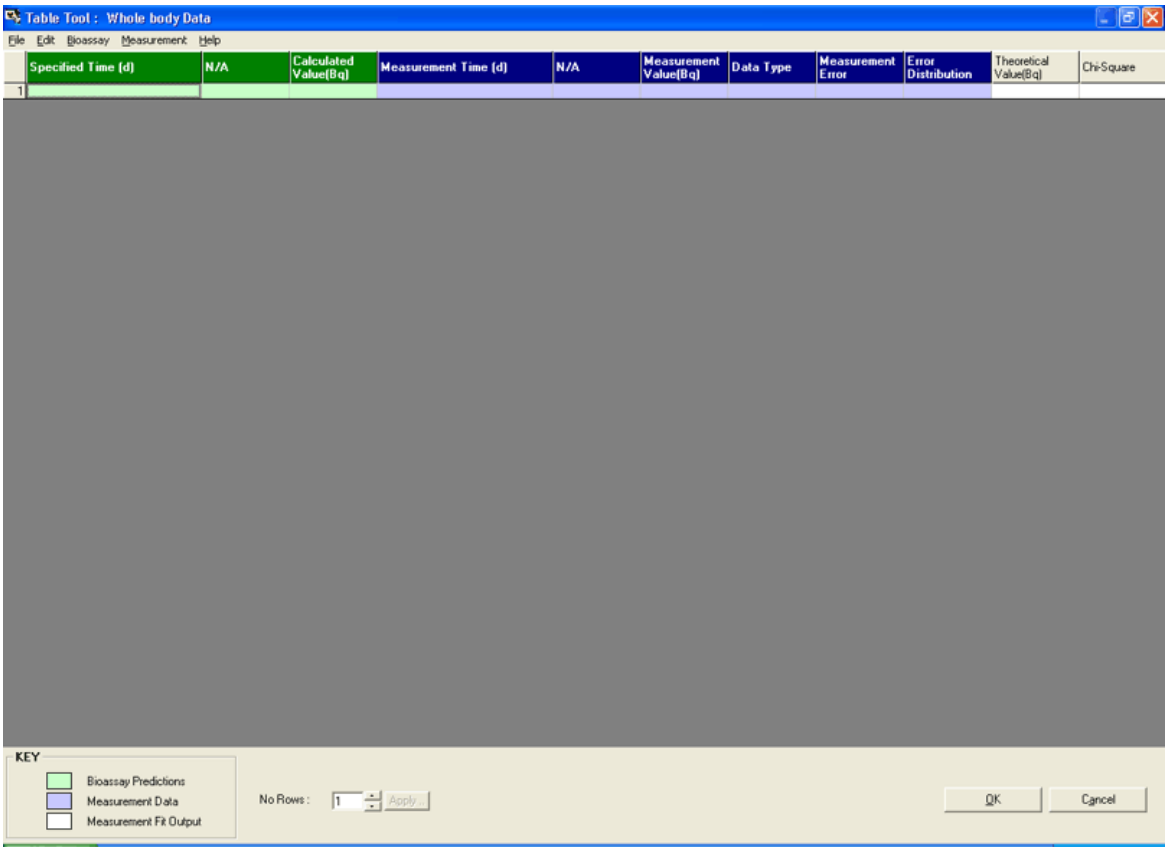


Figure 4.24. Table Tool before data entry - with "**Whole body**" as the Bioassay Quantity.

The **Table Tool** shows all of the data columns (without you having to scroll left and right). When you open this [from a **Bioassay Quantity (BQ)** window], the **Table Tool** will display the same number of rows as the **BQ** window. When opened with a **New** (blank) **Parameter File**, the **default single row** is displayed. Your first task is to open up enough rows to hold all of the **measured bioassay data** that you want to analyze. For example, in the whole-body measurement case with ^{60}Co (Appendix D, Section D.2. – "**Single Intake**"), there are **8** values of whole-body activity. So, in that case you would:

- *Ensure* that you are opening the **Table Tool** from a **Bioassay Quantity** window that is set to show a Table of "**Whole body**" data.
- *Enter* "**8**" in the "**Number of Rows**" dialog box (bottom panel, left-of-center) - see Figure 4.25.
- *Click* the "**Apply**" *button* to the right of the dialog box.

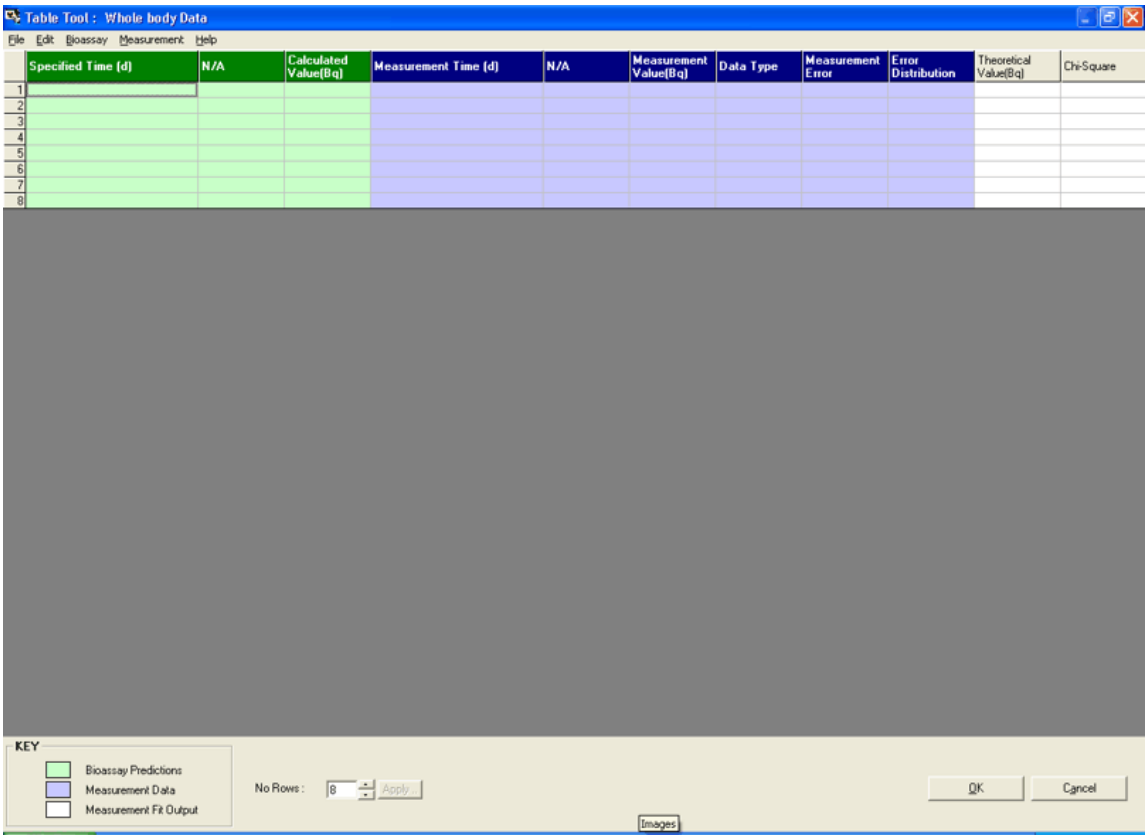


Table 4.25. Table Tool with **8** rows opened.

The data to be entered (in the columns with blue background shown in Figure 4.25) are:

1. **Measurement date** (plus optional **hh:mm**).
2. **N/A column** - *leave* this blank - a "**Collection period**" is **Not Applicable** for whole-body activity.
3. **Measurement value (Bq)**.
4. **Data Type** (**< LOD**, **Real** or **Excluded**).
5. **Measurement Error** - value of the measurement error.
6. **Error Distribution** - type of error distribution (**NORM** or **LOGNORM**).

	Important: Since IMBA Expert™ OCAS/ORAU-Edition uses the **Maximum Likelihood Method** to "fit" the measured data, you MUST complete **all six measurement data columns** (shown with the blue background in Figure 4.25), including appropriate values for the **Data Type**, **Measurement Error**, and **Error Distribution** - for **every data point** (every row displayed in the data table).
	Note: You can specify the **Data Type** - and all other error parameters - **individually for each data point**.

You have three **options** for entering the **measured bioassay data**:

1. *Type* this in **manually** (cell by cell - or block of cells).
2. *Copy* a block of data into the **Table Tool** from a Windows® application using the **Windows® clipboard**.
3. *Read* the data into the **Table Tool** from an **external file**.

4.5.1. Manual Data Entry

4.5.1.1. Data Columns #1 and #3

In this example, the bioassay data to be analyzed are comprised of **8** paired values of **Measurement date** and **Whole-body activity (Bq)** - see **Table 1** in Example of Single Intake Estimation. Each pair of values can be *typed* directly into the **first** and **third** column, respectively, of the **measurement data table** (Figure 4.26).

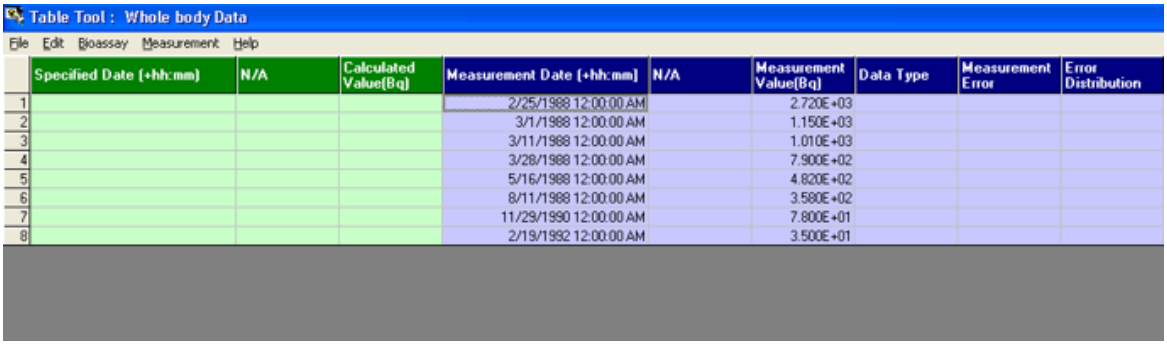


Table Tool : Whole body Data
File Edit Bioassay Measurement Help
Specified Date (+hh:mm) | N/A | Calculated Value(Bq) | Measurement Date (+hh:mm) | N/A | Measurement Value(Bq) | Data Type | Measurement Error | Error Distribution
1 2/25/1988 12:00:00 AM 2.720E+03
2 3/1/1988 12:00:00 AM 1.150E+03
3 3/11/1988 12:00:00 AM 1.010E+03
4 3/28/1988 12:00:00 AM 7.900E+02
5 5/16/1988 12:00:00 AM 4.820E+02
6 8/11/1988 12:00:00 AM 3.580E+02
7 11/29/1990 12:00:00 AM 7.800E+01
8 2/19/1992 12:00:00 AM 3.500E+01

Figure 4.26. *Typing* paired values of **Measurement date** and **Measurement value** into the **Table Tool**.

Tip: All common keyboard and mouse functions, *e.g.*, Backspace, arrow keys, highlight, Delete, **^C** (Copy), **^V** (Paste), will work during manual data entry.

If you now *click* "**OK**" (bottom right-corner of the **Table Tool**) to return to the **Bioassay Quantity** window - and scroll to the right - you will see the values that you have entered displayed in the table (Figure 4.27).

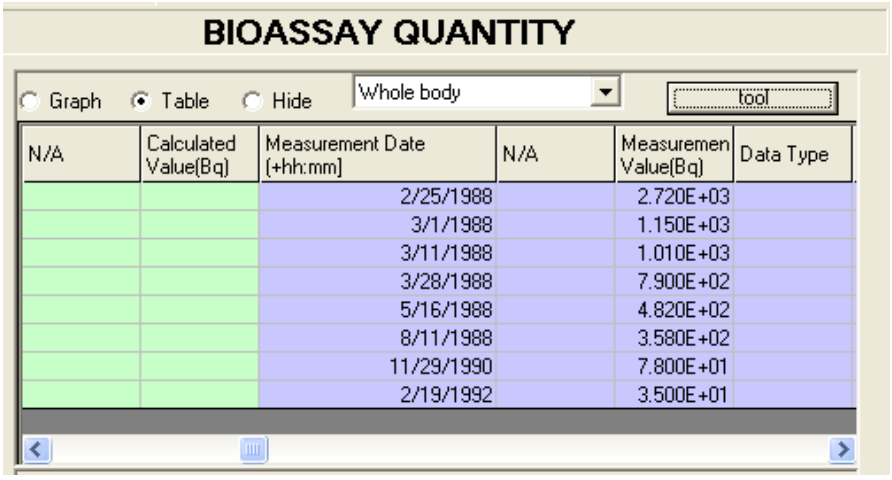
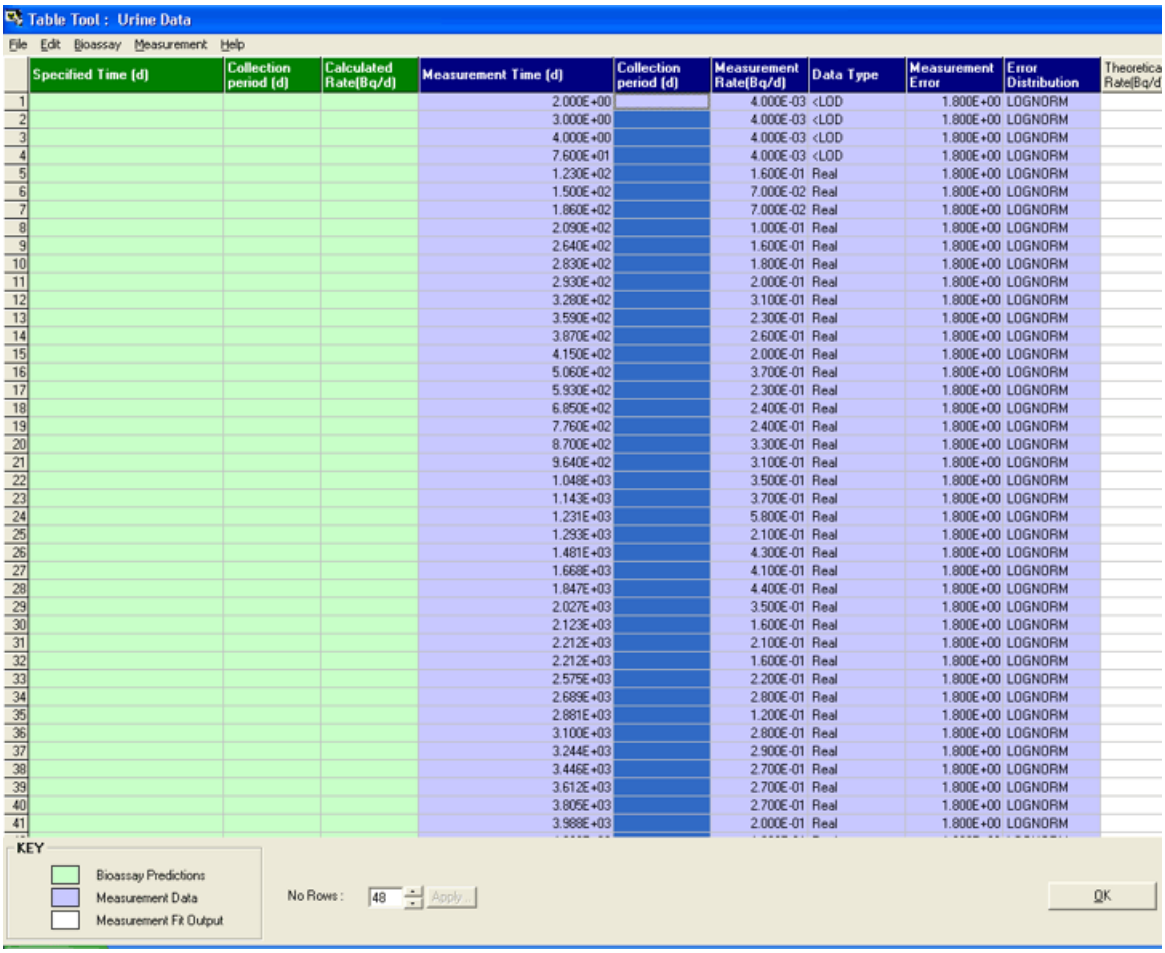


Figure 4.27. Values entered in the **Table Tool** are automatically displayed in the corresponding **Bioassay Quantity** window.

4.5.1.2. Data Column #2

In this example, the **Bioassay Quantity** is "**Whole body**", so **Data Column #2** is not applicable ("**N/A**"). In this case, the IMBA Expert™ OCAS/ORAU-Edition data validation procedure automatically ignores any entries in this column.

If, however, the **Bioassay Quantity** is an **excretion rate** (urinary or fecal), it is necessary to enter the "**Collection Period**" for each sample (**Measurement Value**). The **Table Tool** then provides a **short-cut** for entering repetitive values, *e.g.*, the common collection period of "**1 d**". You simply *highlight* the whole **column** of cells, and type "**1**" - Figure 4.28.



	Specified Time (d)	Collection period (d)	Calculated Rate(Bq/d)	Measurement Time (d)	Collection period (d)	Measurement Rate(Bq/d)	Data Type	Measurement Error	Error Distribution	Theoretica Rate(Bq/d
1				2.000E+00		4.000E-03	<LOD	1.800E+00	LOGNORM	
2				3.000E+00		4.000E-03	<LOD	1.800E+00	LOGNORM	
3				4.000E+00		4.000E-03	<LOD	1.800E+00	LOGNORM	
4				7.600E+01		4.000E-03	<LOD	1.800E+00	LOGNORM	
5				1.230E+02		1.600E-01	Real	1.800E+00	LOGNORM	
6				1.500E+02		7.000E-02	Real	1.800E+00	LOGNORM	
7				1.860E+02		7.000E-02	Real	1.800E+00	LOGNORM	
8				2.090E+02		1.000E-01	Real	1.800E+00	LOGNORM	
9				2.640E+02		1.600E-01	Real	1.800E+00	LOGNORM	
10				2.830E+02		1.800E-01	Real	1.800E+00	LOGNORM	
11				2.930E+02		2.000E-01	Real	1.800E+00	LOGNORM	
12				3.280E+02		3.100E-01	Real	1.800E+00	LOGNORM	
13				3.590E+02		2.300E-01	Real	1.800E+00	LOGNORM	
14				3.870E+02		2.600E-01	Real	1.800E+00	LOGNORM	
15				4.150E+02		2.000E-01	Real	1.800E+00	LOGNORM	
16				5.060E+02		3.700E-01	Real	1.800E+00	LOGNORM	
17				5.930E+02		2.300E-01	Real	1.800E+00	LOGNORM	
18				6.850E+02		2.400E-01	Real	1.800E+00	LOGNORM	
19				7.760E+02		2.400E-01	Real	1.800E+00	LOGNORM	
20				8.700E+02		3.300E-01	Real	1.800E+00	LOGNORM	
21				9.640E+02		3.100E-01	Real	1.800E+00	LOGNORM	
22				1.048E+03		3.500E-01	Real	1.800E+00	LOGNORM	
23				1.143E+03		3.700E-01	Real	1.800E+00	LOGNORM	
24				1.231E+03		5.800E-01	Real	1.800E+00	LOGNORM	
25				1.293E+03		2.100E-01	Real	1.800E+00	LOGNORM	
26				1.481E+03		4.300E-01	Real	1.800E+00	LOGNORM	
27				1.668E+03		4.100E-01	Real	1.800E+00	LOGNORM	
28				1.847E+03		4.400E-01	Real	1.800E+00	LOGNORM	
29				2.027E+03		3.500E-01	Real	1.800E+00	LOGNORM	
30				2.123E+03		1.600E-01	Real	1.800E+00	LOGNORM	
31				2.212E+03		2.100E-01	Real	1.800E+00	LOGNORM	
32				2.212E+03		1.600E-01	Real	1.800E+00	LOGNORM	
33				2.575E+03		2.200E-01	Real	1.800E+00	LOGNORM	
34				2.689E+03		2.800E-01	Real	1.800E+00	LOGNORM	
35				2.881E+03		1.200E-01	Real	1.800E+00	LOGNORM	
36				3.100E+03		2.800E-01	Real	1.800E+00	LOGNORM	
37				3.244E+03		2.900E-01	Real	1.800E+00	LOGNORM	
38				3.446E+03		2.700E-01	Real	1.800E+00	LOGNORM	
39				3.612E+03		2.700E-01	Real	1.800E+00	LOGNORM	
40				3.805E+03		2.700E-01	Real	1.800E+00	LOGNORM	
41				3.988E+03		2.000E-01	Real	1.800E+00	LOGNORM	

Figure 4.28. Entering the same value in a *highlighted* block of cells.

Tip: *Highlight* the **whole** data column with a single click - by *right-clicking* the column **heading** - "**Collection Period (d)**" in this case.

4.5.1.3. Data Column #4

In this example, all **8** measured values are "**Real**" data, *i.e.*, **finite** measured values. Therefore, "**Real**" must be entered in all cells of the fourth data column. IMBA Expert™ OCAS/ORAU-Edition provides a further **short-cut** for doing this in the **Table Tool** (Figure 4.29):

- *highlight* the whole of the fourth data column;
- *right-click* on any *highlighted* cell - the drop-down menu will automatically appear (Figure 7.6);
- *select* "**Real**" from the drop-down menu.

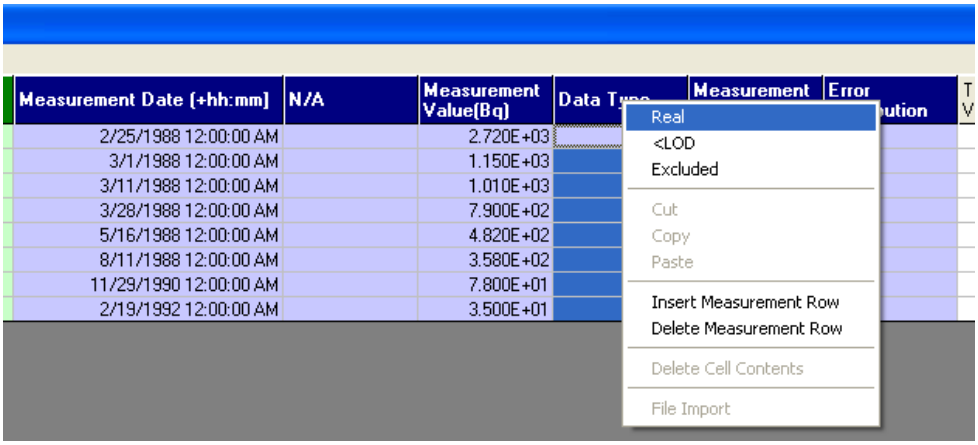


Figure 4.29. Drop-down menu for entering the "**Data Type**."

This will enter "**Real**" in all of the *highlighted* cells (Figure 4.30).

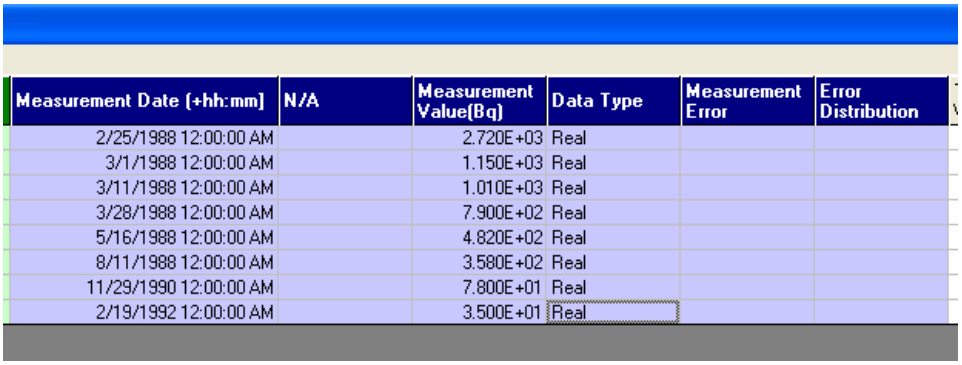


Figure 4.30. Entering the "**Data Type**" in all cells of data column #4.

4.5.1.4. Data Column #5

In this example, there are **no explicit measurement** errors. However, in order to apply the **Maximum Likelihood Method** to "**fit**" the data, an explicit **error weighting** MUST be defined for every data point. Again, IMBA Expert™ OCAS/ORAU-Edition provides a **short-cut** for doing this in the **Table Tool**. This gives you the option of applying:

- a **Uniform Absolute** error;
- a **Uniform Relative** error;
- a **Square Root** error.

In this example, the measured values vary over a large range (from 2720 Bq to 35 Bq). For accurate dosimetry, it is as important to "fit" the small values, as it is to fit the initial high values. In this case, it is reasonable to apply a **Uniform Relative** error to all data points. To do this you simply:

- *highlight* the whole of the fifth data column;
- *right-click* on any *highlighted* cell;
- *select* "**Generate Errors**" - Figure 4.31.

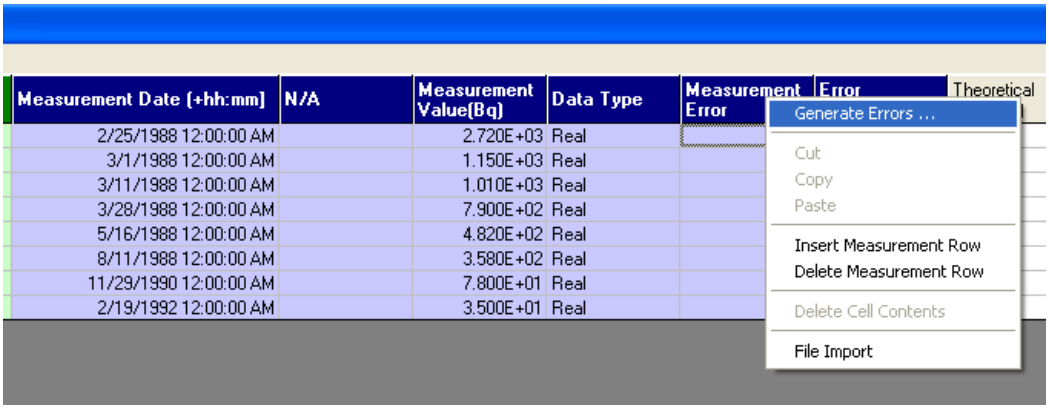


Figure 4.31. Drop-down menu to "**Generate Errors**."

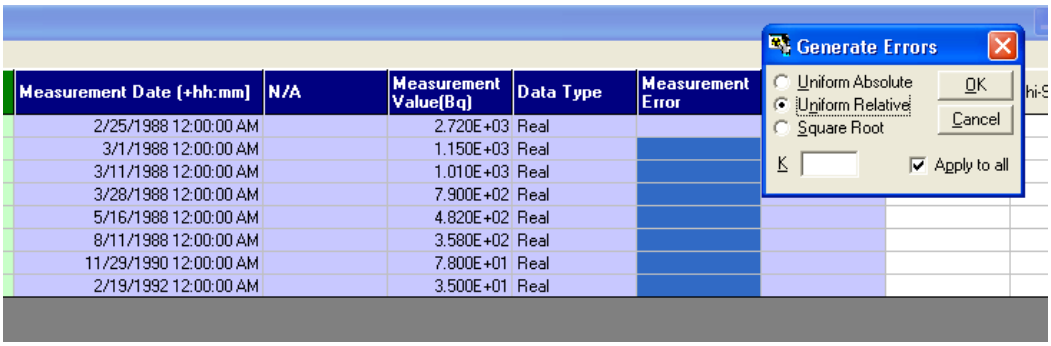


Figure 4.32. The "Generate Errors" window.

In the "generate Errors" window:

- "**Uniform Relative**" error is *set* by default - or *select* alternative;
- "**Apply to all**" measurement values is *set* by default - or *un-check* to apply to a *selected* range of measurement values;
- the value of the "**Error Constant**" ("**K**") must be entered.

For a **Uniform Relative** error, the chosen value of "**K**" (when applied to ALL measurement values) has no effect on the fitted value - since all data points are given a proportional error-weighting. "**K**" can be any **non-zero** value. The value "**0.1**" is a convenient **default**.

When you *click* the "**OK**" button to *apply* your selected value of "**K**" you will be warned that "**This will overwrite the measurement errors**" - and you will be given an opportunity to change your mind (Figure 4.33).

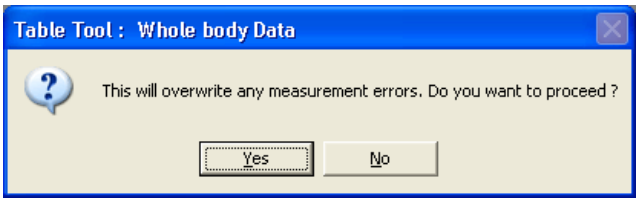


Figure 4.33. Warning message before overwriting measurement errors.

4.5.1.5. Data Column #6

The final data column defines the type of **Error Distribution** for each error value. This is either:

- **NORM** - normal (Gaussian), or;
- **LOGNORM** - lognormal.

To enter the type of **Error Distribution** for all **8** error values (Figure 4.34):

- *highlight* all of the cells in data column #6 - this will automatically display the **Error Distribution** menu;
- *select* "**NORM**" - to specify a **Normal** error distribution for all errors.

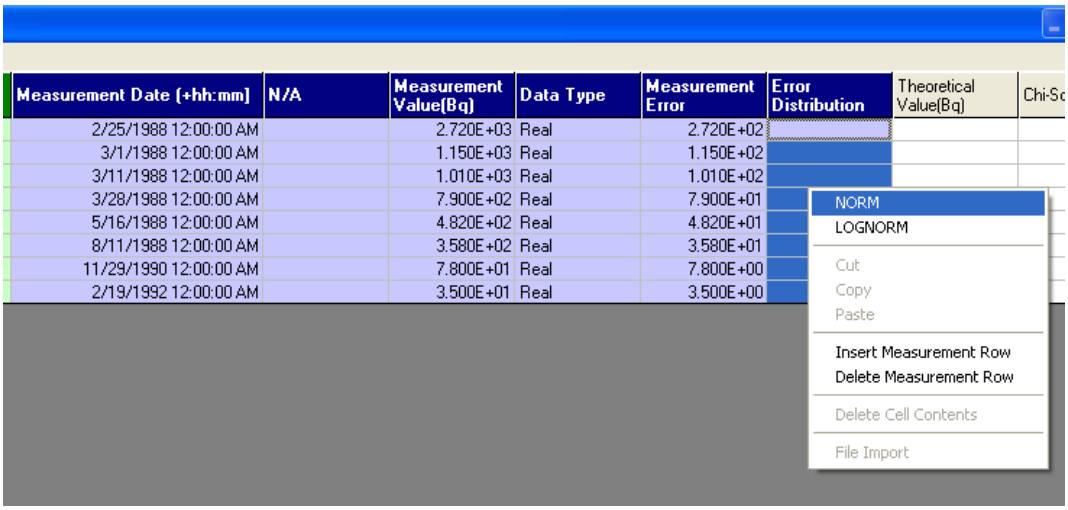


Figure 4.34. Selecting a **Normal** distribution for each error value.

"**NORM**", signifying a "**Normal**" distribution of errors, will then be entered automatically in all *highlighted* cells of data column #6 (Figure 4.35).

Measurement Date (+hh:mm)	N/A	Measurement Value(Bq)	Data Type	Measurement Error	Error Distribution	TH Va
2/25/1988 12:00:00 AM		2.720E+03	Real	2.720E+02	NORM	
3/1/1988 12:00:00 AM		1.150E+03	Real	1.150E+02	NORM	
3/11/1988 12:00:00 AM		1.010E+03	Real	1.010E+02	NORM	
3/28/1988 12:00:00 AM		7.900E+02	Real	7.900E+01	NORM	
5/16/1988 12:00:00 AM		4.820E+02	Real	4.820E+01	NORM	
8/11/1988 12:00:00 AM		3.580E+02	Real	3.580E+01	NORM	
11/29/1990 12:00:00 AM		7.800E+01	Real	7.800E+00	NORM	
2/19/1992 12:00:00 AM		3.500E+01	Real	3.500E+00	NORM	

Figure 4.35. Completed measurement data in **Table Tool**.

4.5.1.6. Completed Data Table in Bioassay Quantity Window

Figure 4.36 shows the resulting completed **table of measurement data**, as it appears in the corresponding **Bioassay Quantity** window.

BIOASSAY QUANTITY

Graph Table Hide Whole body tool

Measurement Date (+hh:mm)	N/A	Measuremen Value(Bq)	Data Type	Measuremen Error	Error Distribution
2/25/1988		2.720E+03	Real	2.720E+02	NORM
3/1/1988		1.150E+03	Real	1.150E+02	NORM
3/11/1988		1.010E+03	Real	1.010E+02	NORM
3/28/1988		7.900E+02	Real	7.900E+01	NORM
5/16/1988		4.820E+02	Real	4.820E+01	NORM
8/11/1988		3.580E+02	Real	3.580E+01	NORM
11/29/1990		7.800E+01	Real	7.800E+00	NORM
2/19/1992		3.500E+01	Real	3.500E+00	NORM

Figure 4.36. Completed **Bioassay Quantity** table of data.

Tip: *Right-clicking* on any cell in the data table enables you to "**Insert**" or "**Delete**" a **whole row** of measurement data. This automatically **opens** a new "blank" row (below the row that you *clicked* on), or **deletes** the row that you *clicked* on, respectively. This does NOT interfere with any rows of values in the first three columns of the **Table Tool** (with green background), which relate to the "**predicted**" bioassay values. The "green" and "blue" columns of the **Table Tool** operate independently.

4.5.2. Using the Clipboard

4.5.2.1. Importing a Block of Data

You can very easily *enter* your bioassay measurement data into the **Table Tool** using the Windows® clipboard:

1. *highlight* the required column(s) of data in your source Windows® application (Figure 4.37);
2. *copy* the highlighted block of data;
3. *open* the **Table Tool** for the appropriate bioassay quantity;
4. *click* on destination cell for the copied data block - this will automatically show the "**Paste**" menu (Figure 4.38);
5. *paste* the block of data.

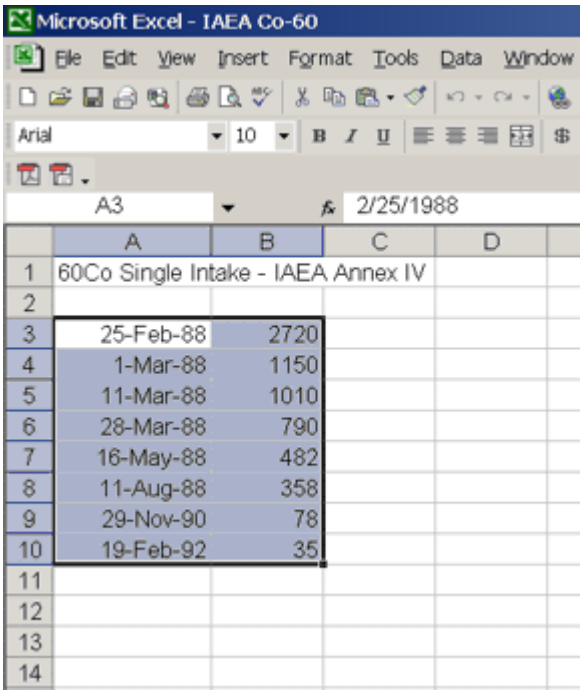


Figure 4.37. Highlighting a block of data in Microsoft Excel spreadsheet for copying to the Windows® clipboard.

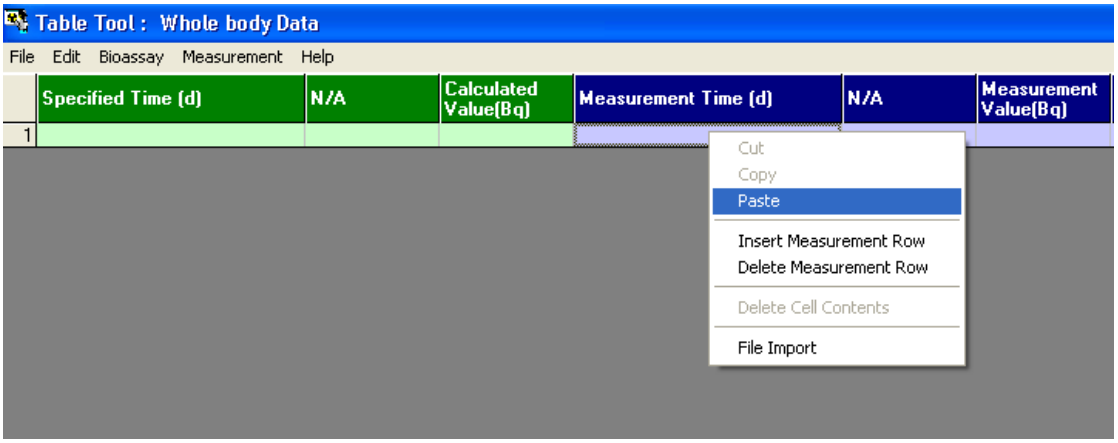


Figure 4.38. Clicking on the **destination** cell in the **Table Tool** shows the "**Paste**" menu.

To *paste* the block of data from the Windows® clipboard to the destination cell in the **Table Tool**, you can use:

- the "**Paste**" *button* on a Microsoft Office-type keyboard;
- **^V** (control paste);
- "**Paste**" in the drop-down menu (Figure 4.38).

You will see the following **Warning** notice (Figure 4.39). If you click "**Yes**", the **Table Tool** will *open* a sufficient number of rows (below your insertion level) to accommodate your pasted data (Figure 4.40).

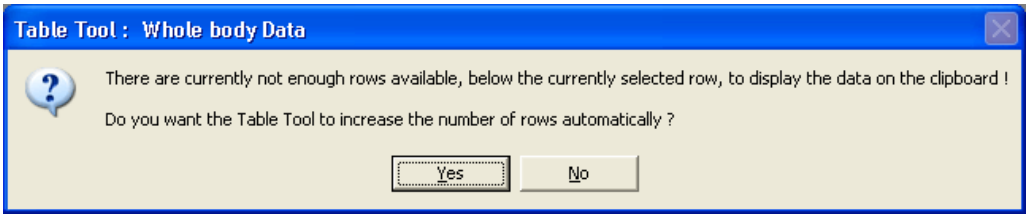
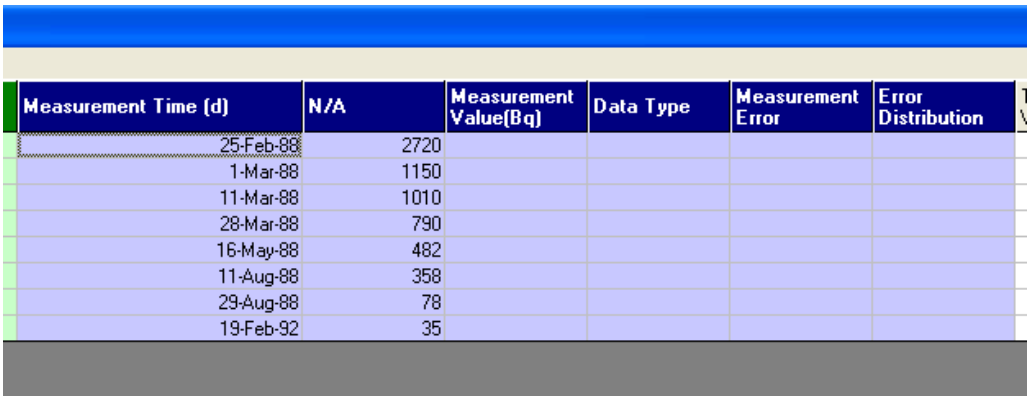


Table Tool : Whole body Data
There are currently not enough rows available, below the currently selected row, to display the data on the clipboard !
Do you want the Table Tool to increase the number of rows automatically ?
Yes
No

Figure 4.39. Warning notice.



Measurement Time (d)	N/A	Measurement Value(Bq)	Data Type	Measurement Error	Error Distribution
25-Feb-88	2720				
1-Mar-88	1150				
11-Mar-88	1010				
28-Mar-88	790				
16-May-88	482				
11-Aug-88	358				
29-Aug-88	78				
19-Feb-92	35				

Figure 4.40. Block of data *pasted* into the destination cell (top-left) of the **Table Tool**.

Notice in Figure 4.40 above, that the **measurement values** were pasted into the next column to the right of "**Measurement Date (+hh:mm)**." In this case, they need to be *moved* (manually) to the correct "**Measurement Value (Bq)**" column:

- *click* on the "**N/A**" (incorrect) column heading - to *highlight* the **whole** column of data to be moved;
- *right-click* on any highlighted cell - the "**Cut/Copy**" menu will appear (Figure 4.41);
- *click* "Cut" - this will put the column of data into the clipboard;
- *click* the "**Measurement Value (Bq)**" column heading - this will *highlight* all of the "target" cells in this column;
- *right-click* on any target cell - the "**Paste**" menu will automatically appear (Figure 4.42);
- *click* "**Paste**".

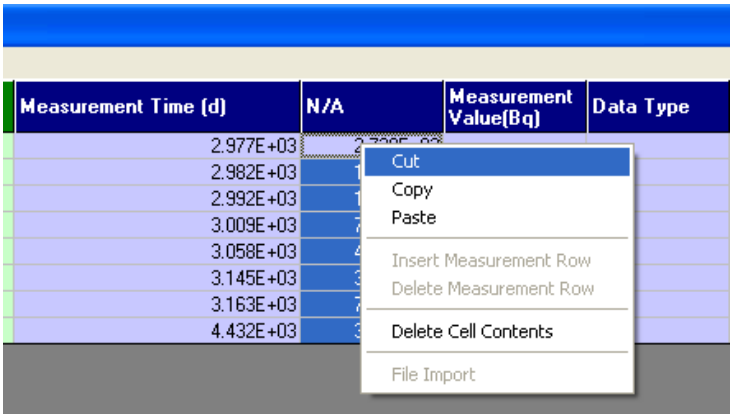


Figure 4.41. Moving a column of data in the **Table Tool**.

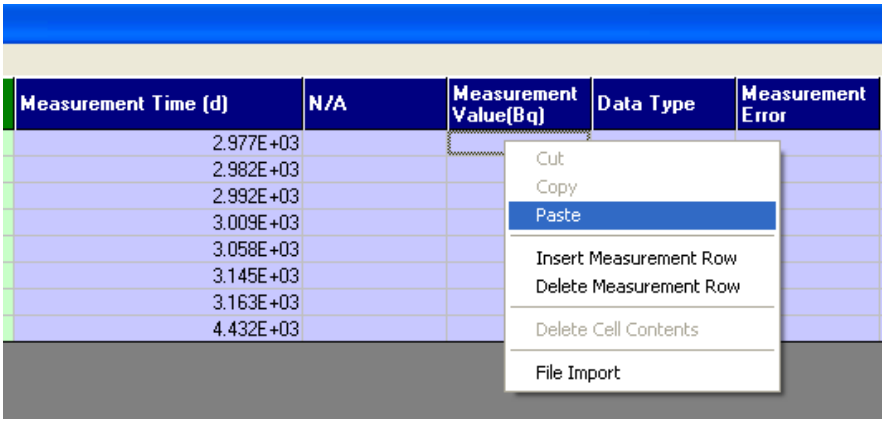


Figure 4.42. Pasting data to the target cells.

Key Tip: The drop-down menu that appears when you *right-click* anywhere in the **Table Tool** is "**context sensitive**" - *i.e.*, it automatically shows you only those options that are applicable to the *clicked* cell.

4.5.2.2. Completing the Remaining Data Columns

Enter the data required for the **remaining four columns** (blue background) using the **tools** already described to facilitate manual data entry. These columns are:

- **Collection Period (d)** - this is not applicable (**N/A**) for **Whole Body** as the bioassay quantity.
- **Data Type** - either < LOD, Real or Imaginary.
- **Measurement Error** - value of the error for each measurement.
- **Error Distribution** - either Normal or Lognormal.

4.5.3. Importing from a Data Text File

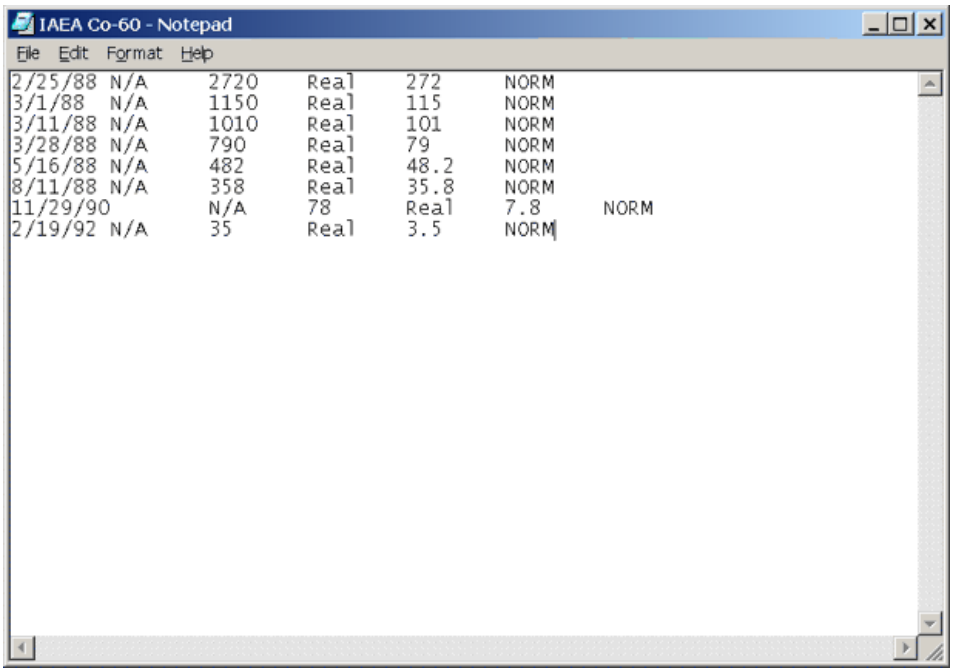

IAEA Co-60 - Notepad
File Edit Format Help
2/25/88 N/A 2720 Real 272 NORM
3/1/88 N/A 1150 Real 115 NORM
3/11/88 N/A 1010 Real 101 NORM
3/28/88 N/A 790 Real 79 NORM
5/16/88 N/A 482 Real 48.2 NORM
8/11/88 N/A 358 Real 35.8 NORM
11/29/90 N/A 78 Real 7.8 NORM
2/19/92 N/A 35 Real 3.5 NORM

Figure 4.43. Tab delimited text file ("**IAEA Co-60.txt**") holding measurement data.

You can import data directly into the **Table Tool** from an **ASCII text file** with the following types of delimiter:

- **comma** separated values;
- **tab** delimited values;
- **space** delimited values;
- **your own definition** of the delimiter.

To import your data:

- *right-click* on the **destination cell** for your imported text file data (Figure 4.44) - the "**File Import**" menu will appear;
- *click* "**File Import**".

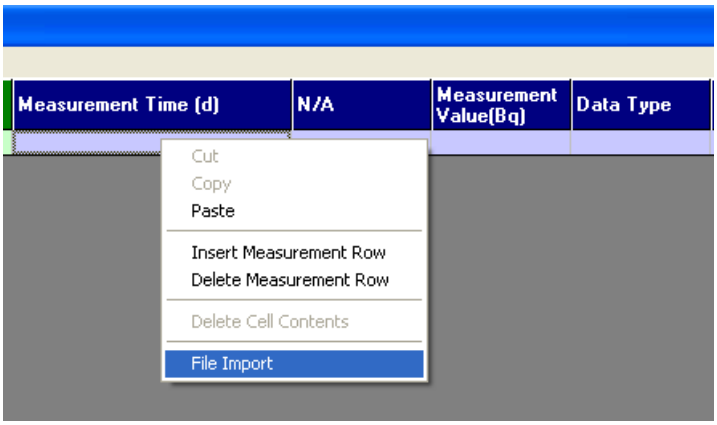


Figure 4.44. "**File Import**" menu.

The message shown in Figure 4.45 will appear - to remind you to check that you are importing the file into the correct location in the Table.

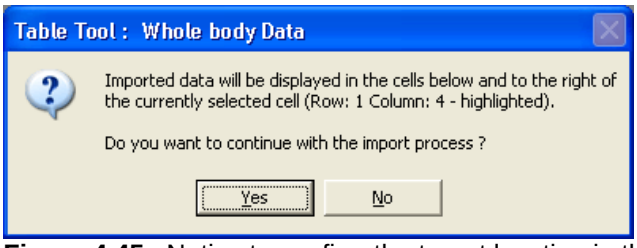


Table Tool : Whole body Data
Imported data will be displayed in the cells below and to the right of the currently selected cell (Row: 1 Column: 4 - highlighted).
Do you want to continue with the import process ?
Yes
No

Figure 4.45. Notice to confirm the target location in the data table.

Click "**Yes**" to *open* the "**ASCII file import wizard**" (Figure 4.46). Use the wizard to:

- *browse* to the ASCII text file containing your measurement data;
- *view* the data file - Figure 4.47;
- *select* the appropriate type of data delimitation - "**Tab delimited**" in this example.

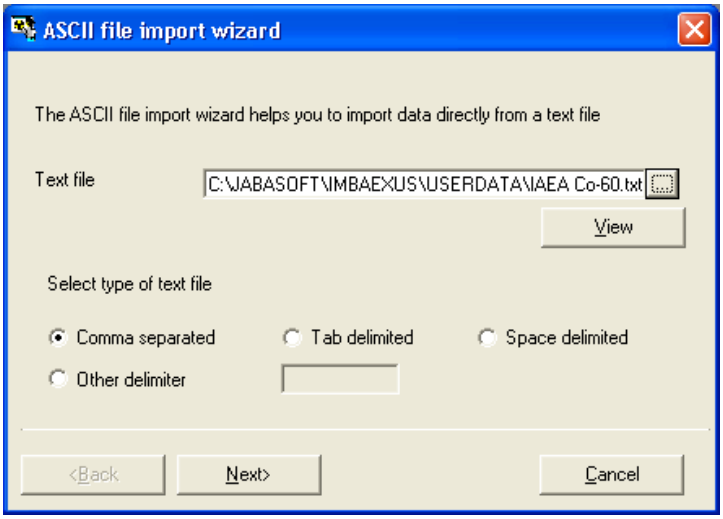


Figure 4.46. ASCII file import wizard for browsing to the **data text file** containing measurement data.

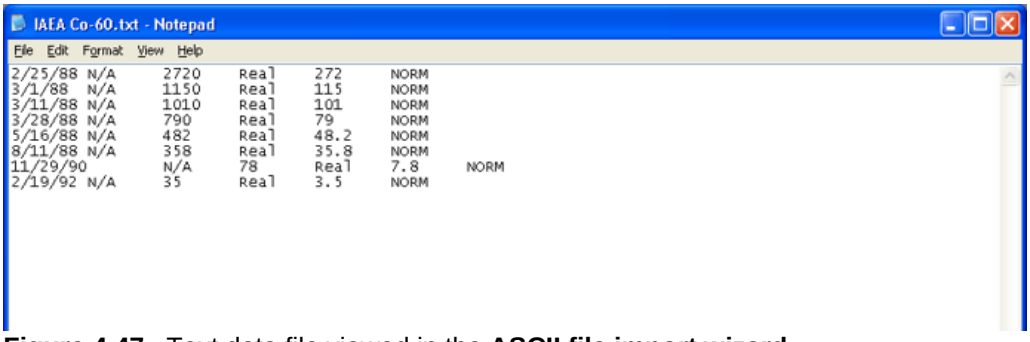

IAEA Co-60.txt - Notepad
File Edit Format View Help
2/25/88 N/A 2720 Real 272 NORM
3/1/88 N/A 1150 Real 115 NORM
3/11/88 N/A 1010 Real 101 NORM
3/28/88 N/A 790 Real 79 NORM
5/16/88 N/A 482 Real 48.2 NORM
8/11/88 N/A 358 Real 35.8 NORM
11/29/90 N/A 78 Real 7.8 NORM
2/19/92 N/A 35 Real 3.5 NORM

Figure 4.47. Text data file viewed in the **ASCII file import wizard**.

Clicking "**Next**" in the **ASCII file import wizard** enables you to *select* (by *highlighting*) the data that you wish to **import** into the **Table Tool** (Figure 4.48). *Click* the "**Select All**" *button* to select all of the **whole ASCII text file**. Once you have selected the data that you want to import into the **Table Tool**, *click* "**Next**" (Figure 4.49).

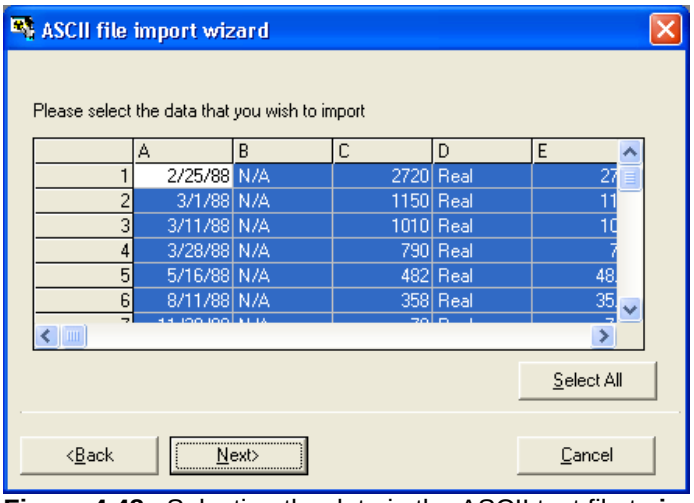


Figure 4.48. Selecting the data in the ASCII text file to **import** into the **Table Tool**.

Click "**Next**". You will be given an opportunity to change your mind about pasting the selected data - which will overwrite any existing data in the target cells of the **Table Tool** (Figure 4.50).

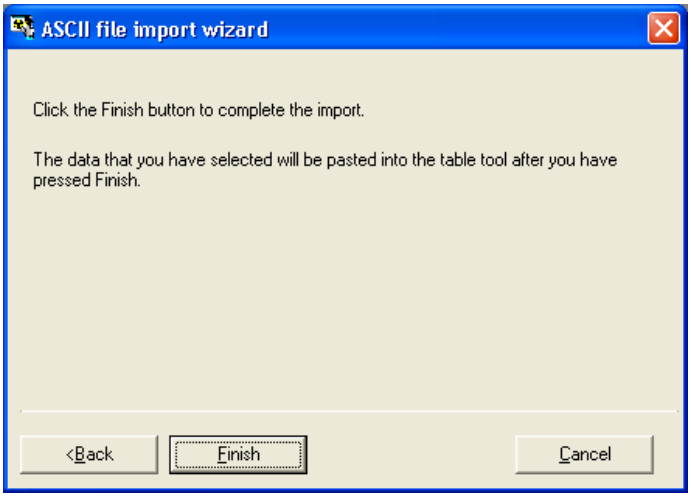

ASCII file import wizard
Click the Finish button to complete the import.
The data that you have selected will be pasted into the table tool after you have pressed Finish.
<Back
Finish
Cancel

Figure 4.49. Reminder that you are about to paste data into the Table Tool.

Click "**Finish**" to proceed with your data import (Figure 4.50) - or "**Cancel**" this.

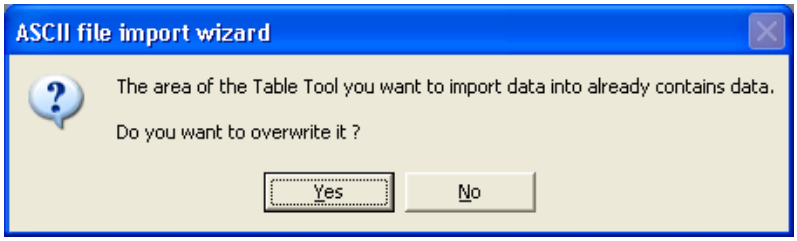
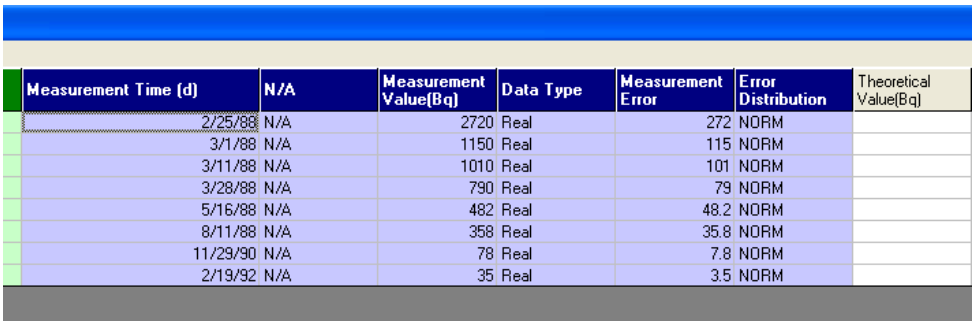

ASCII file import wizard
The area of the Table Tool you want to import data into already contains data.
Do you want to overwrite it ?
Yes
No

Figure 4.50. Warning that you are about to overwrite existing data in the target cells.

To *complete* the importation of your selected data, *click* "**Yes**". This will automatically write your **imported data** to the target cells of the **Table Tool**, starting in the first row of the first measurement data column (blue background), as shown in Figure 4.51.



Measurement Time (d)	N/A	Measurement Value(Bq)	Data Type	Measurement Error	Error Distribution	Theoretical Value(Bq)
2/25/88	N/A	2720	Real	272	NORM	
3/1/88	N/A	1150	Real	115	NORM	
3/11/88	N/A	1010	Real	101	NORM	
3/28/88	N/A	790	Real	79	NORM	
5/16/88	N/A	482	Real	48.2	NORM	
8/11/88	N/A	358	Real	35.8	NORM	
11/29/90	N/A	78	Real	7.8	NORM	
2/19/92	N/A	35	Real	3.5	NORM	

Figure 4.51. Data successfully imported into the **Table Tool**.

If there are **not enough rows open** in the **Table Tool** to hold your data, you will be **warned** (Figure 4.52).

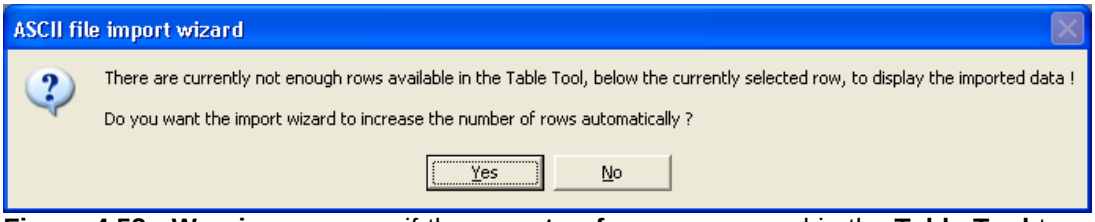
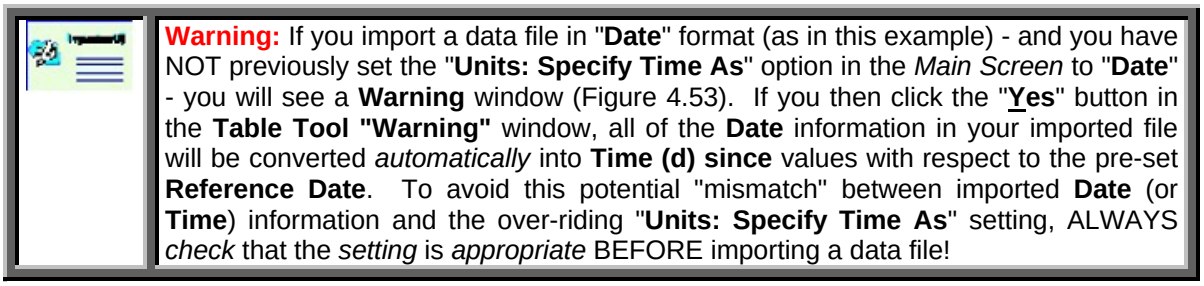

ASCII file import wizard
There are currently not enough rows available in the Table Tool, below the currently selected row, to display the imported data !
Do you want the import wizard to increase the number of rows automatically ?
Yes
No

Figure 4.52. Warning message if there are **too few rows** opened in the **Table Tool** to receive imported data.

In this case, *click* "**Yes**" to automatically *add* the required number of new rows to the table - and *import* the *highlighted* data from the **external file**. Then *click* the "**OK**" button in the **Table Tool** to return to the *Bioassay Calculations Screen*.



Warning: If you import a data file in "**Date**" format (as in this example) - and you have NOT previously set the "**Units: Specify Time As**" option in the *Main Screen* to "**Date**" - you will see a **Warning** window (Figure 4.53). If you then click the "**Yes**" button in the **Table Tool "Warning"** window, all of the **Date** information in your imported file will be converted *automatically* into **Time (d) since** values with respect to the pre-set **Reference Date**. To avoid this potential "mismatch" between imported **Date** (or **Time**) information and the over-riding "**Units: Specify Time As**" setting, ALWAYS *check* that the *setting* is *appropriate* BEFORE importing a data file!

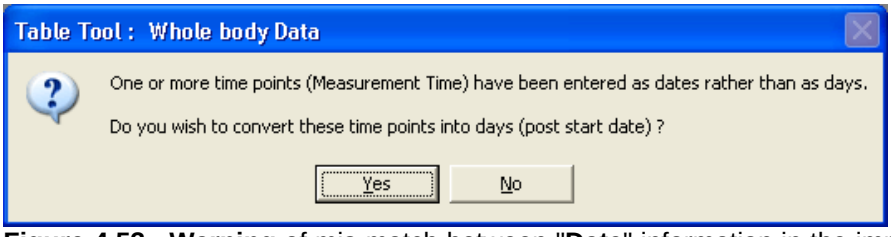


Table Tool : Whole body Data
One or more time points (Measurement Time) have been entered as dates rather than as days.
Do you wish to convert these time points into days (post start date) ?
Yes
No

Figure 4.53. Warning of mis-match between "**Date**" information in the imported file and the pre-set "**Time**" option.

In this example, provided that your previous "**Units: Specify Time As**" option was correctly set at "**Date**", your imported data will appear in the designated **Bioassay Quantity** window, as shown in Figure 4.54.

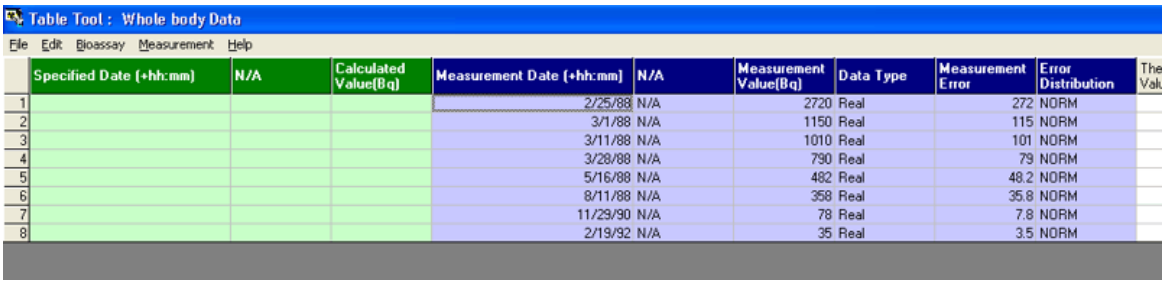


Table Tool : Whole body Data
File Edit Bioassay Measurement Help
Specified Date (+hh:mm) N/A Calculated Value(Bq) Measurement Date (+hh:mm) N/A Measurement Value(Bq) Data Type Measurement Error Error Distribution
1 2/25/88 N/A 2720 Real 272 NORM
2 3/1/88 N/A 1150 Real 115 NORM
3 3/11/88 N/A 1010 Real 101 NORM
4 3/28/88 N/A 790 Real 79 NORM
5 5/16/88 N/A 482 Real 48.2 NORM
6 8/11/88 N/A 358 Real 35.8 NORM
7 11/29/90 N/A 78 Real 7.8 NORM
8 2/19/92 N/A 35 Real 3.5 NORM

Figure 4.54. Imported data as it appears in the **Bioassay Quantity** window.

Important: IMBA Expert™ OCAS/ORAU-Edition automatically **converts all dates** in the imported file to **your international setting**. In the example above, the dates in the imported text file were already in the "U.S." convention. If, however, you send your data file (or parameter file) to a European (or other international) User, your data will be converted *automatically* to the User's own "country" convention when it is written to the **Bioassay Quantity** window by their software (IMBA Professional Plus).

4.5.4. Data Validation

Data validation is first performed automatically in the **Table Tool** after the "**OK**" button is *clicked*. While validation is being performed, the mouse pointer displays an hourglass icon. For large data sets, a status bar is displayed (Figure 4.55). The validation tests performed are:

1. Data in columns is assumed to be part of a continuous set of data - and scrutinized by the validation procedure from the first (top) cell until an empty cell is encountered.
2. Any cell data encountered after an empty cell is ignored by the validation process.
3. The validation routine will halt at the first cell encountered in the data grid that contains invalid data. A message box is displayed, and the offending cell is *highlighted*.

The criteria for invalid data are:

1. Non-numerical data in cells expected to contain numerical input.
2. Data that cannot be converted to a valid date/time value in cells expected to contain date/time.
3. Columns for "**Collection Period**" are validated only for urinary or fecal bioassay quantities.

If the data validation is successful, the mouse pointer icon reverts to the default, and the **Table Tool** form is hidden.

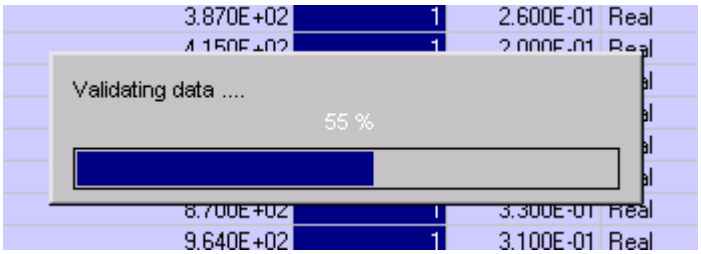


Figure 4.55. Data Validation.

Tip: The "**validation**" feature, whereby IMBA Expert™ OCAS/ORAU-Edition ignores all data entered below an "**empty**" cell, allows you to enter additional information relating to a dataset (but not part of the analysis) - below the data set.

A second, more rigorous, validation is performed automatically before any calculation, to ensure that all data values are sensible.

4.6. Graph Tool for Viewing the Data and Fit

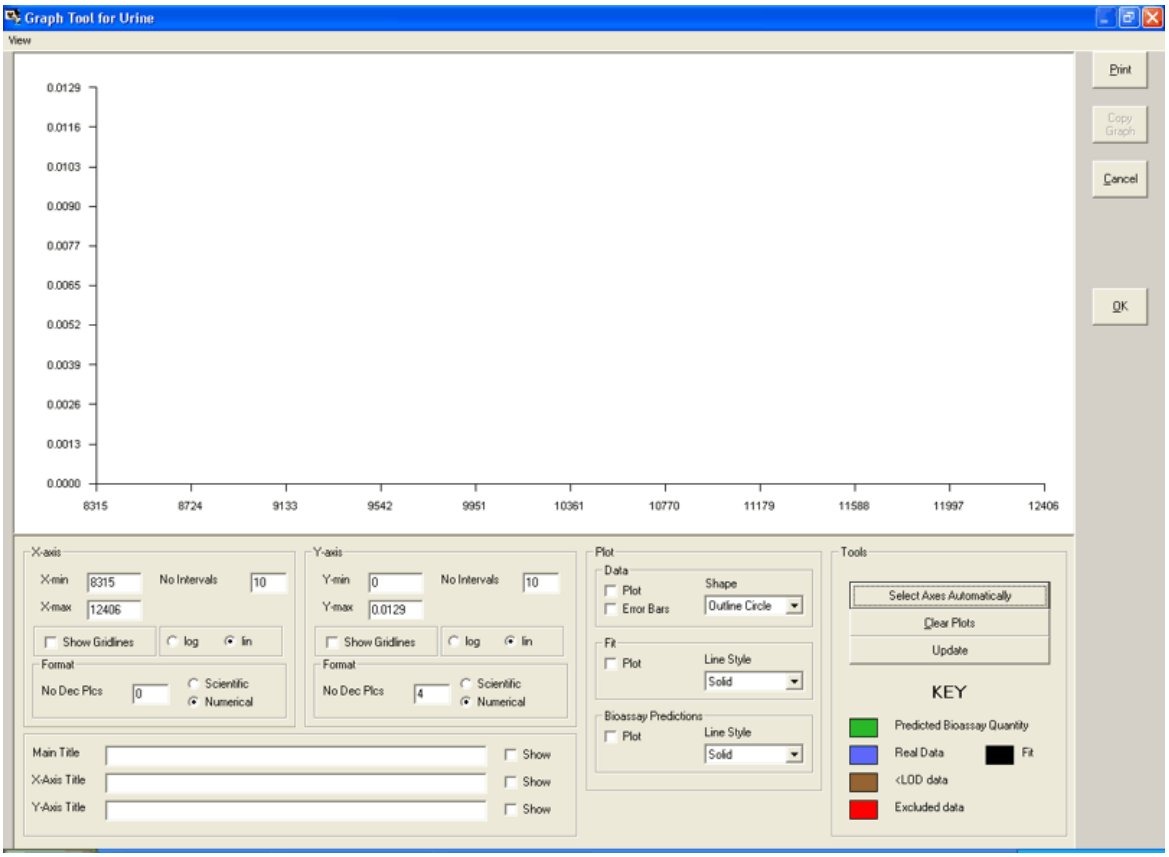


Figure 4.56. Selecting Axes Automatically in the **Graph Tool**.

In the "**Tools**" sub-panel, *click* **Select Axes Automatically** (Figure 4.56). This will set up the range of the X- and Y-axes to include **all of the data points**.

To *plot* the data points with their error bars (as in Figure 4.57):

- *select* "**Outline Circle**" for the **Shape** of the **data symbol** ("**Plot**" sub-panel);
- *check* the "**Plot**" *box*;
- *check* the "**Error Bars**" *box.*

As you *check* each *box*, the respective symbol is plotted automatically (Figure 4.57).

In the example shown (Figure 4.57), the following "**User**" selections have been made for the Y-axis:

- **Scientific** scale;
- "**1**" decimal place;
- "**3**" intervals.

You can also **select** the **scale** of the **X-axis**, the appearance of **plotted symbols**, and the "**Line Style**" of the plotted "**Fit**" and "**Bioassay Predictions**."

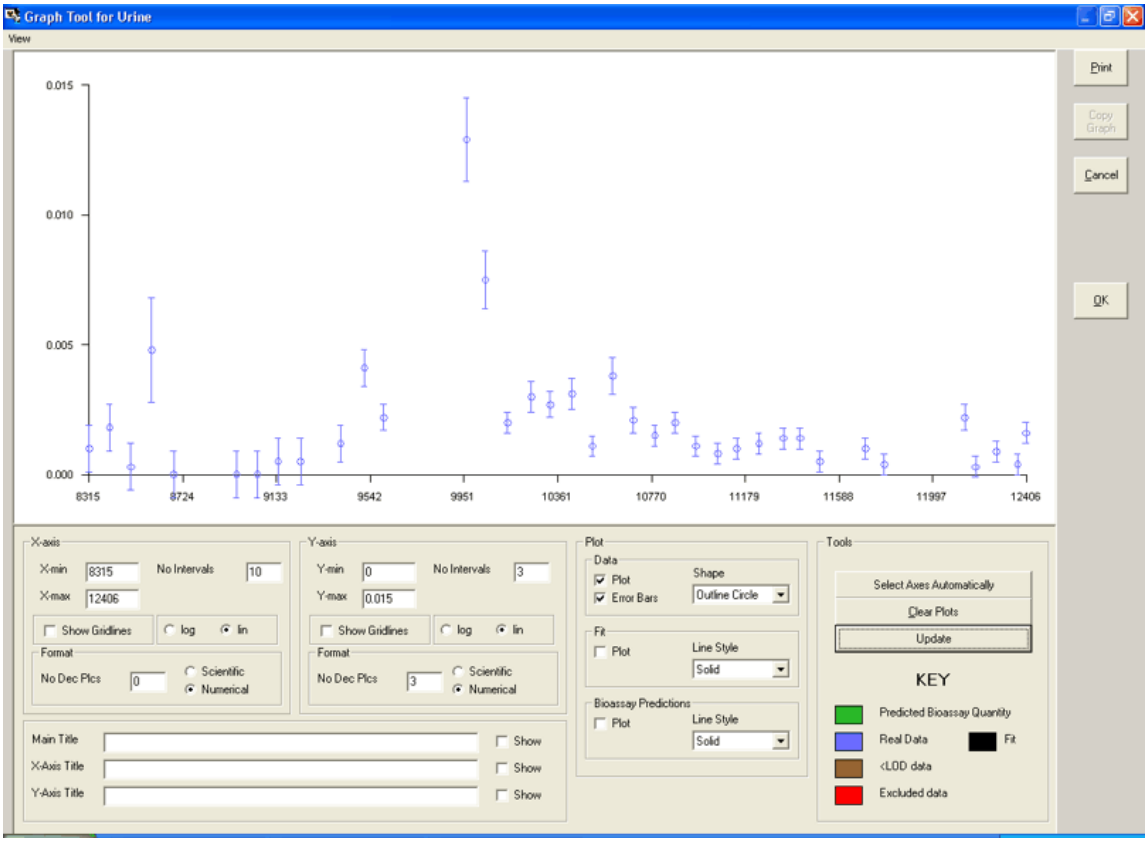


Figure 4.57. Plotting the **data points** and **error bars**.

Tip: Before you leave the **Graph Tool**, *check* the "**Plot**" **box** under the heading "**Fit**." This will automatically plot the **fit to the data** (in both the **Graph Tool** and the linked **Bioassay Quantity** window) - when you *calculate* the **maximum likelihood estimate** of the **Intake** amount(s).

Click the "**OK**" *button* (right-side panel) to close the **Graph Tool** - and return to the **Bioassay Quantity** windows. The **graph** of the **data and error bars** will then be displayed in the opened **graph window** (Figure 4.58).

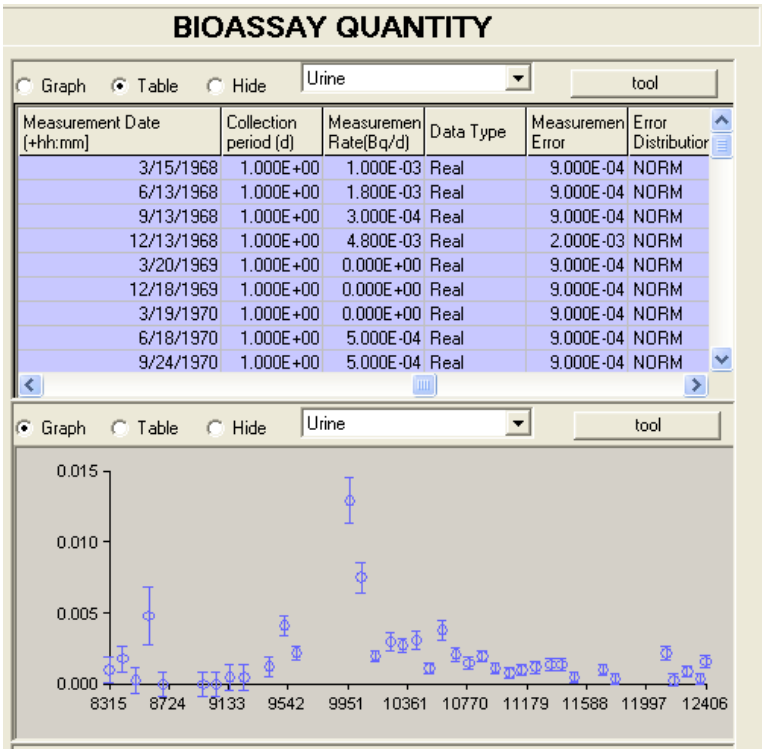


Figure 4.58. Graph of Whole body **data and error bars** displayed in **Bioassay Quantity** window.

4.6.1. Maximizing and Exporting the Graph

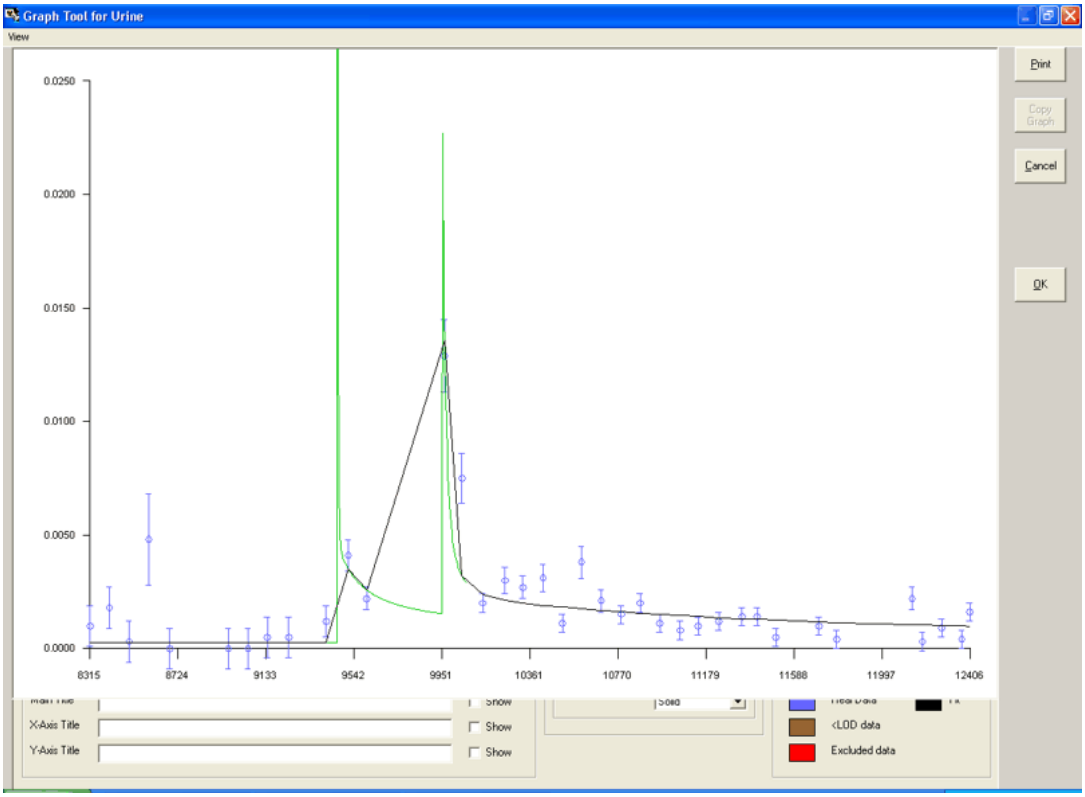


Figure 4.59. Maximized view of the **Graph**.

Clicking **View | Maximize** (from the **View** menu, top-left corner of the **Graph Tool** window) maximizes the graph plot so that you can view this in finer detail, as shown in Figure 4.59.

	Tip #1: Use the **Ctrl/Alt/Print Scrn** keys (together) to send the "maximized" image of the graph to the Windows® clipboard. You can then **paste** this image directly into another Windows® application file, *e.g.*, a **report** being prepared in a word processor.
	Tip #2: If you wish to "crop" the graph image to show only the plot itself (and not the background parts of the key etc.), you must currently use a separate "graphics" application to do this. The "**Copy Graph**" feature will be included in a future version – to enable you to export just the graph plot.

5. Dose Calculations Screen

The **Dose Calculations** screen (Figure 5.1) opens when you **click** the **"Dose Calculations" button** (on the **Main Screen**).

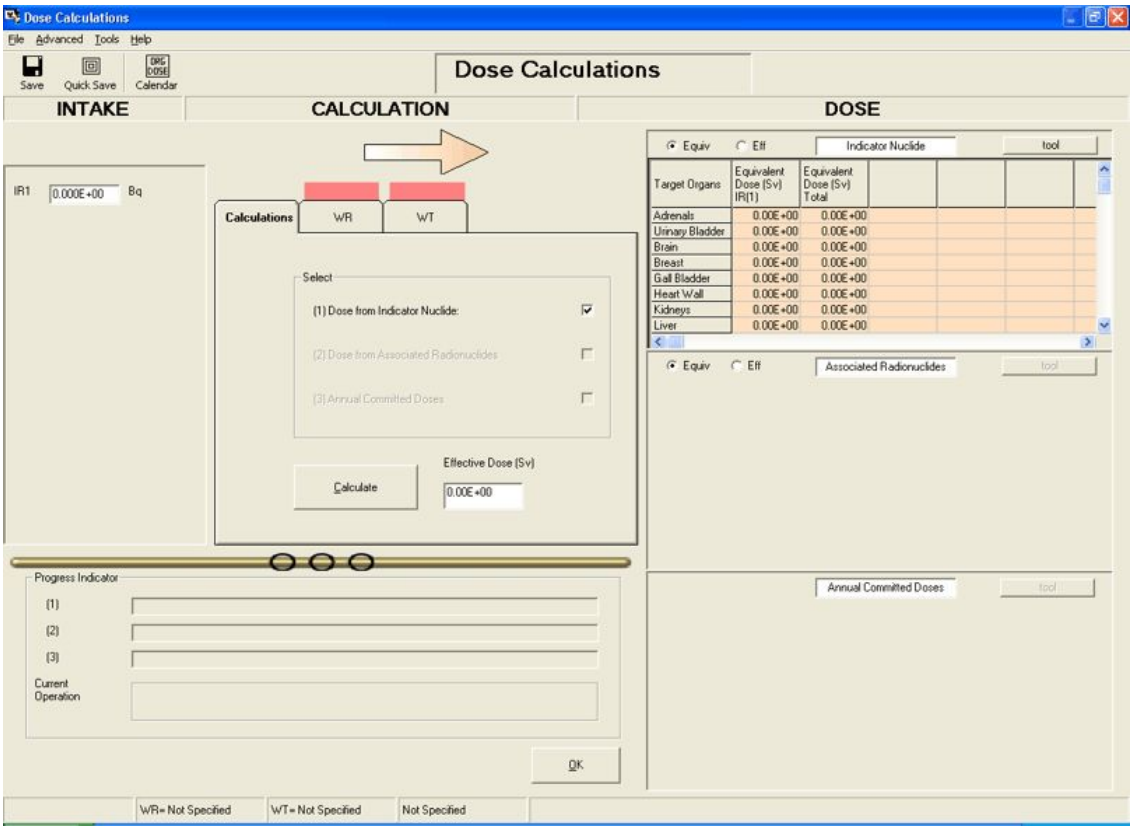


Figure 5.1. The **Dose Calculations** screen.

The screen is divided into these functional parts:

- **Menu Bar** – including access to the special calculations of **annual dose received by target organs** (required by **NIOSH** for application to **EEOICPA**).
- **Intake** sub-panel.
- **Calculation** sub-panel.
- **Calculation Progress Indicator**.
- **Dose Results** windows.

5.1. Dose Calculations Menus

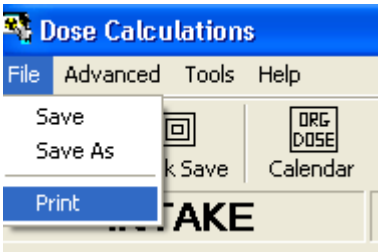


Figure 5.2. Dose Calculations Menus.

These are:

- the **File** menu - to **Save/Save As** all parameter values to a **Parameter File** (*via* the Windows® browser), or **Print** a screenshot of the entire "**Dose Calculations Screen**";
- the Advanced menu – to open "**Advanced Dosimetry Options**";
- the Tools menu – to open the "**Equivalent Dose to selected organ received in each calendar year**" window;
- the **Help** menu - giving access to all Help facilities (except the Check for Updates **Wizard**).

Note: The calculations performed directly in the **Dose Calculations** screen are for committed dose, as needed for regulatory purposes, *e.g.*, to meet the requirements of 10 CFR 835. The special calculations of annual equivalent dose received by designated target organs required by **NIOSH** (for application to EEOICPA) - which are accessed via the **Dose Calculations | Tools** menu - are described later.

5.2. Dose Calculation Tools

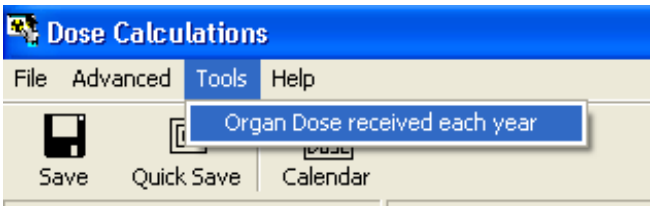


Figure 5.3. Tool to calculate "**Organ Doses Received in Each Calendar Year**".

This special IMBA Expert™ OCAS/ORAU-Edition Tool enables doses received by specified organs to be evaluated - for input to the **NIOSH-IREP** (causation probability calculation) software.

- Use of this tool is described after the general operation of the IMBA Expert™ software - in the section of the **User Manual** entitled 'Special EEOICPA Applications'.

5.3. Intake Sub-panel – for Dose Calculations

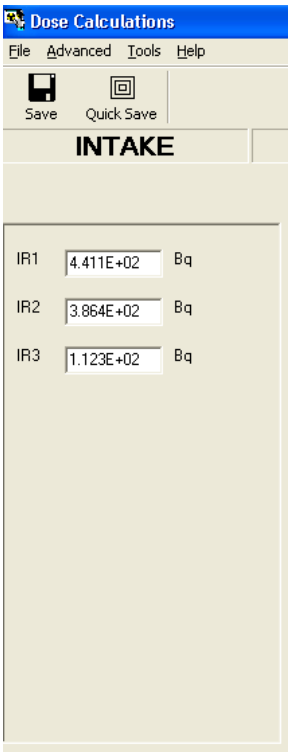


Figure 5.4. Intake sub-panel.

The **Intake** sub-panel shown in Figure 5.4 is displaying the calculated amounts of three intakes (IR1, IR2 and IR3). These values are the result of the Example of Estimating Multiple Intakes using the *Miller et al. (1999)* data. You can also enter *hypothetical* values of *intake*, or values from other sources, directly in the **Intake** dialog boxes.

5.4. Dose Calculation Progress Indicator

To *calculate* (and display) the resulting doses, *check* the required calculation(s), and *click* the "**Calculate**" *button*. If you have forgotten to *specify* the **Biokinetic Model** for the **Indicator Nuclide**, you will see the **Warning Notice** shown in Figure 5.5. Once you have *selected* the **Biokinetic Model**, the dose calculation will proceed automatically.

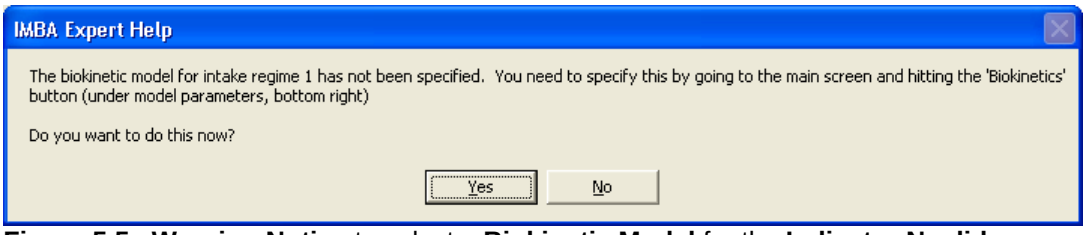

IMBA Expert Help
The biokinetic model for intake regime 1 has not been specified. You need to specify this by going to the main screen and hitting the 'Biokinetics' button (under model parameters, bottom right)
Do you want to do this now?
Yes
No

Figure 5.5. Warning Notice to select a **Biokinetic Model** for the **Indicator Nuclide**.

Note: For all **Associated Radionuclides**, IMBA Expert™ OCAS/ORAU-Edition automatically selects the **currently recommended ICRP biokinetic model**.

The **Progress Indicator** (Figure 5.6) displays which part of the calculation is currently being performed, and when the final dose calculations are complete. All calculations are sequenced and performed automatically. In the example shown in Figure 5.6, IMBA Expert™ OCAS/ORAU-Edition is calculating the numbers of radioactive disintegrations in each source organ resulting from the third intake (**IR3**) - for the **Indicator Nuclide** - the first *checked* calculation.

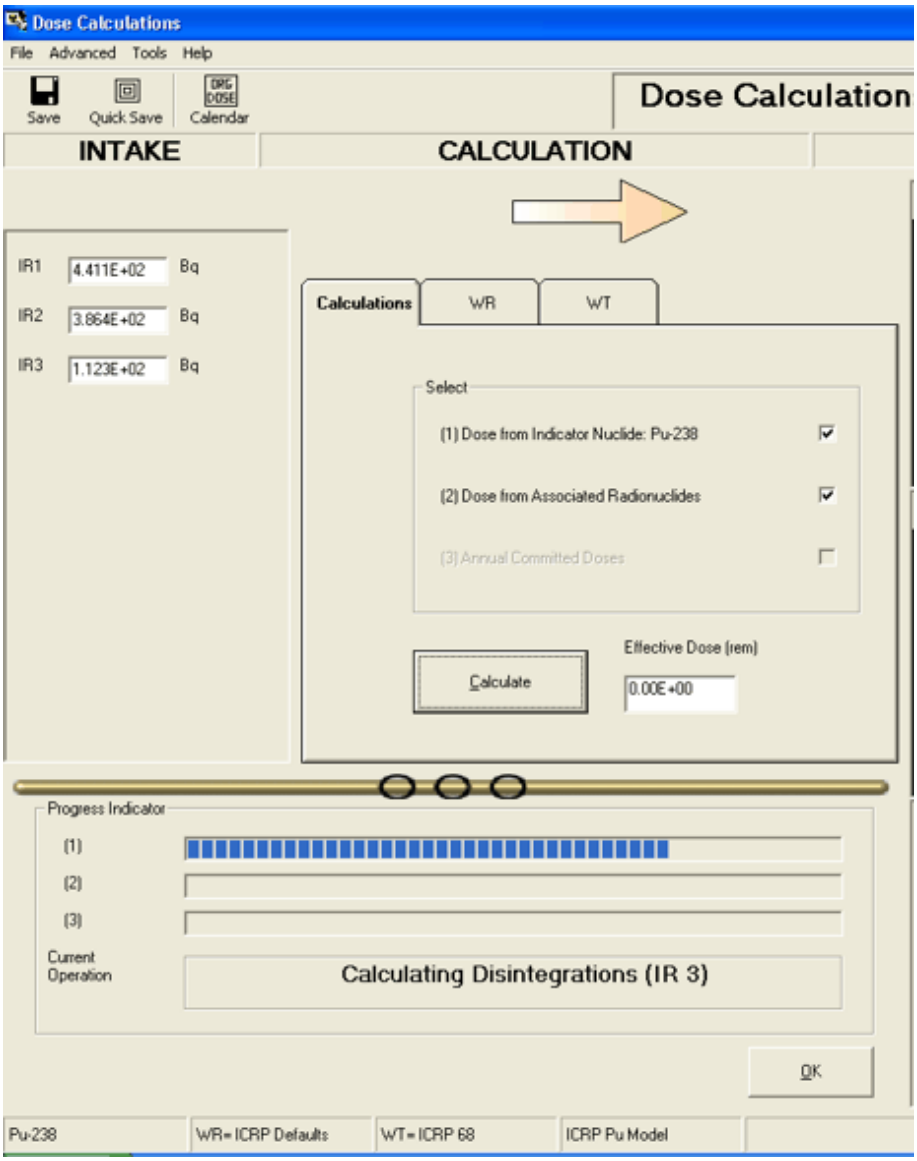


Figure 5.6. Progress Indicator shows what calculation is currently being performed.

5.5. Dose Results Window

Figure 5.7 shows the results for **Equivalent Dose** displayed in two windows:

- **Indicator Radionuclide** window - for each separate **Intake Regime** (**IR**), together with the **Total Equivalent Dose** from all intake regimes to each **Target Organ**;
- **Associated Radionuclide** window - for each **Associated Radionuclide**, together with the **Total Equivalent Dose** from all associated radionuclides to each **Target Organ**.

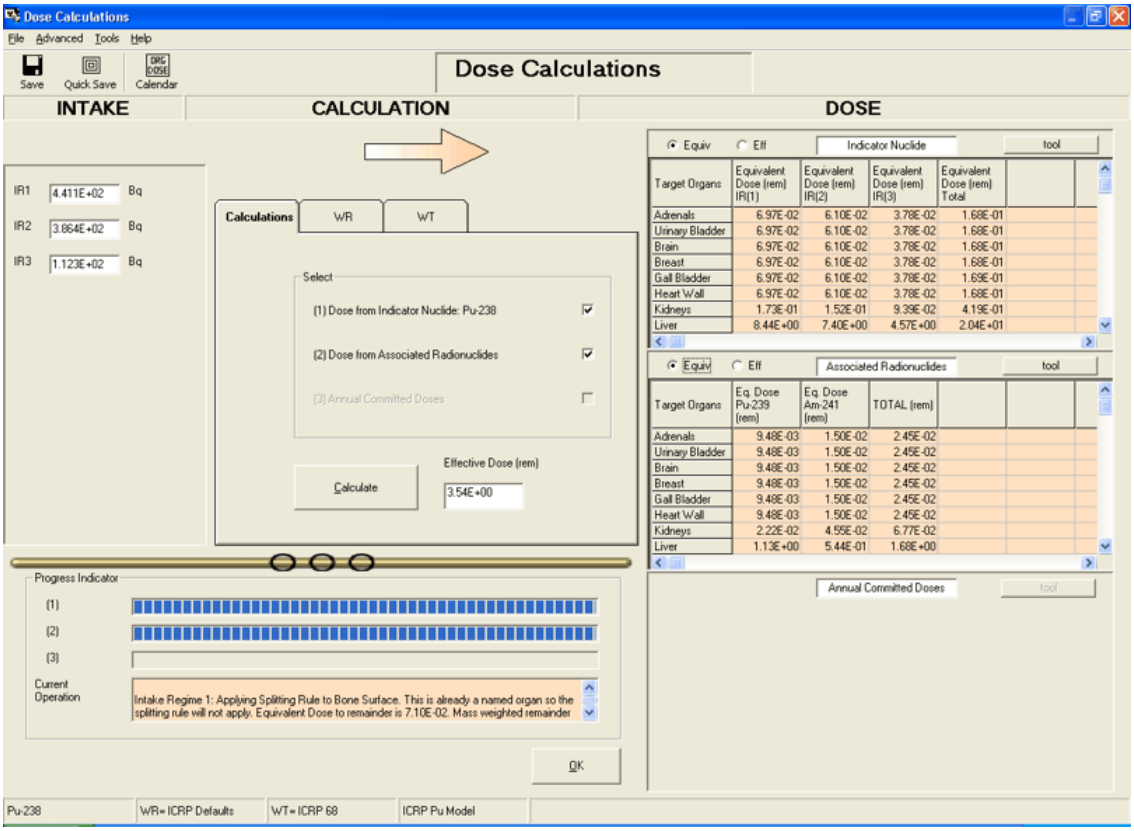


Figure 5.7. Displayed results of a completed **Dose Calculation** set to show **Equivalent Doses** in the "**Dose**" windows.

You can *toggle* the "**Equiv/Eff**" selector for either window to switch the display instantly between **Equivalent Dose** and **Effective Dose**. Figure 5.8 shows both window displays switched to **Effective Dose**.

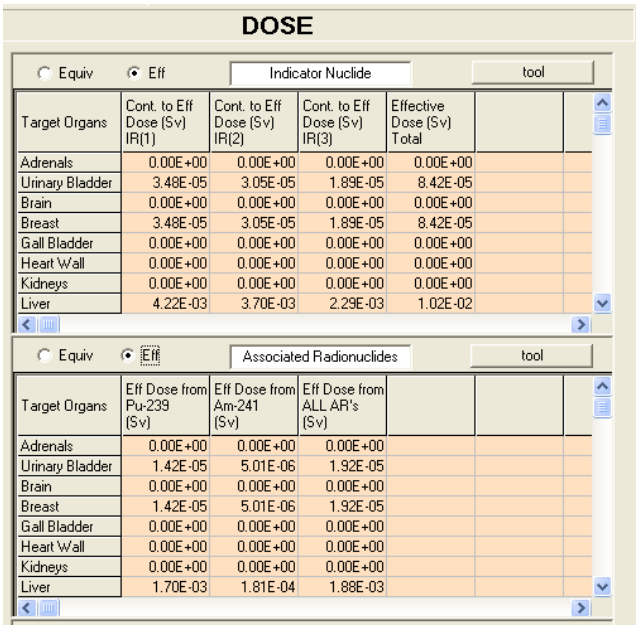

DOSE
Equiv Eff
Indicator Nuclide
tool
Target Organs
Cont. to Eff Dose (Sv) IR(1)
Cont. to Eff Dose (Sv) IR(2)
Cont. to Eff Dose (Sv) IR(3)
Effective Dose (Sv) Total
Adrenals 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Urinary Bladder 3.48E-05 3.05E-05 1.89E-05 8.42E-05
Brain 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Breast 3.48E-05 3.05E-05 1.89E-05 8.42E-05
Gall Bladder 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Heart Wall 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Kidneys 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Liver 4.22E-03 3.70E-03 2.29E-03 1.02E-02
Equiv Eff
Associated Radionuclides
tool
Target Organs
Eff Dose from Pu-239 (Sv)
Eff Dose from Am-241 (Sv)
Eff Dose from ALL AR's (Sv)
Adrenals 0.00E+00 0.00E+00 0.00E+00
Urinary Bladder 1.42E-05 5.01E-06 1.92E-05
Brain 0.00E+00 0.00E+00 0.00E+00
Breast 1.42E-05 5.01E-06 1.92E-05
Gall Bladder 0.00E+00 0.00E+00 0.00E+00
Heart Wall 0.00E+00 0.00E+00 0.00E+00
Kidneys 0.00E+00 0.00E+00 0.00E+00
Liver 1.70E-03 1.81E-04 1.88E-03

Figure 5.8. Displayed results of a completed **Dose Calculation** set to show **Effective Doses** in the "**Dose**" windows.

Note: During a calculation, the dialog box labeled "**Effective Dose (Sv)**" in Figure 5.8 displays first the **Effective Dose** calculated for the **Indicator Nuclide** - as soon as this result is available. Once the calculations are completed for the **Associated Radionuclide(s)**, the total **Effective Dose** from the latter is automatically **added** to that from the **Indicator Nuclide**, and the result (overall total) is displayed in the dialog box.

5.5.1. Dose Committed in Each Calendar Year

This feature is not available in IMBA Expert™ OCAS/ORAU-Edition.

5.6. Dose Calculations Sub-panel

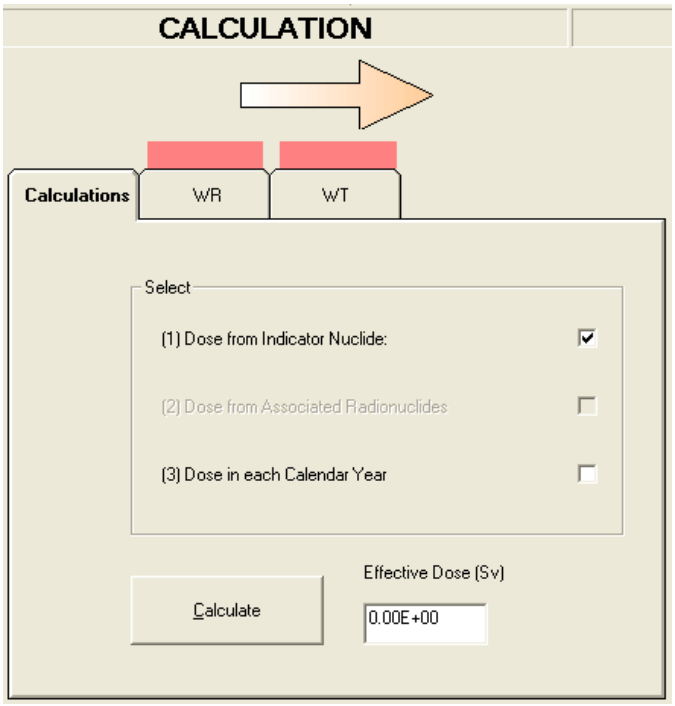


Figure 5.9. Dose Calculation sub-panel at start-up.

Figure 5.9 shows the **Dose Calculation** sub-panel as it appears for a **New** case (blank **Parameter File**). Note the red flags above the "**WR**" and "**WT**" tabs, signifying that neither the **Radiation Weighting Factors** nor the **Tissue Weighting Factors** to be used in the dose calculation have yet been defined. Also, no **Indicator Nuclide** has yet been defined - signified by the absence of a named radionuclide in the "**(1) Dose from Indicator Nuclide**" label.

5.6.1. Dose from Associated Radionuclides

Taking the *Miller et al. (1999)* case as an example (**Appendix D: Example Bioassay Cases – "Estimating Multiple Intakes"** – Section D.3.), let's assume that each intake of ^{238}Pu was associated with two additional radionuclides, ^{239}Pu and ^{241}Am. Let's hypothesize that the ^{239}Pu activity concentration in the inhaled material was 15% of the indicator ^{238}Pu value, and the ^{241}Am activity concentration 5%. These values are set up in the **Associated Radionuclides** sub-panel of the **Main Screen**, as shown in Figure 5.10.

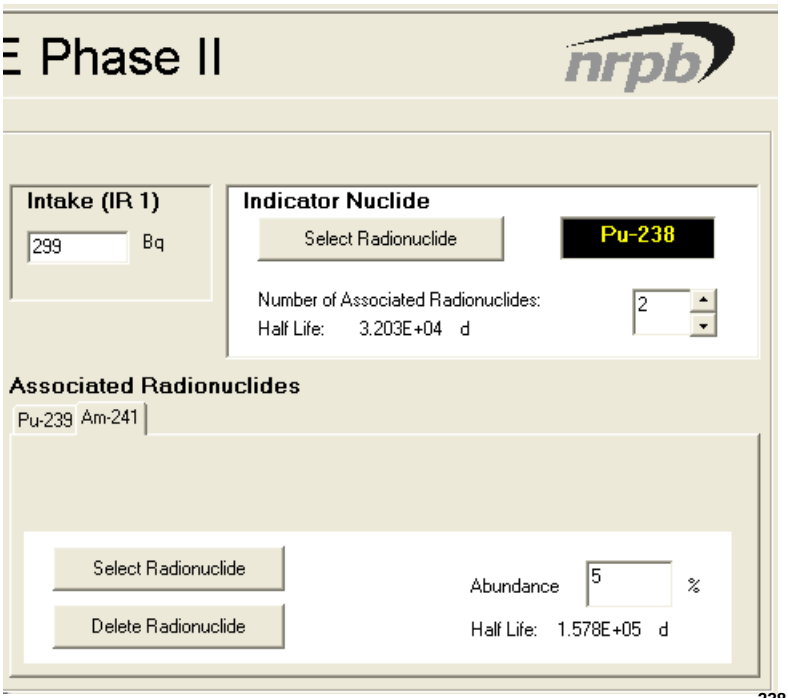


Figure 5.10. Example of two **Associated Radionuclides**, with ^{238}**Pu** as the **Indicator Nuclide**.

For this example, the **Dose Calculation** sub-panel will appear as shown in Figure 5.11. Note that a second checkbox is now activated - for "**(2) Dose from Associated Radionuclides**".

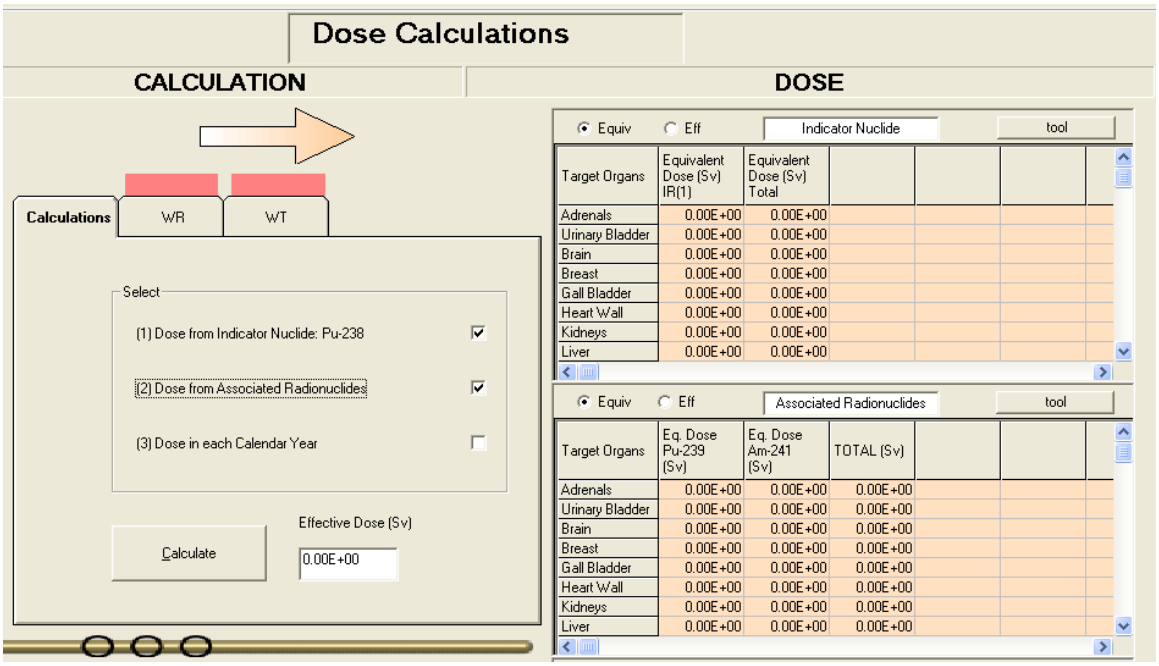


Figure 5.11. Dose Calculation sub-panel for case with **Associated Radionuclides**.

5.6.2. Defining the Radiation Weighting Factors

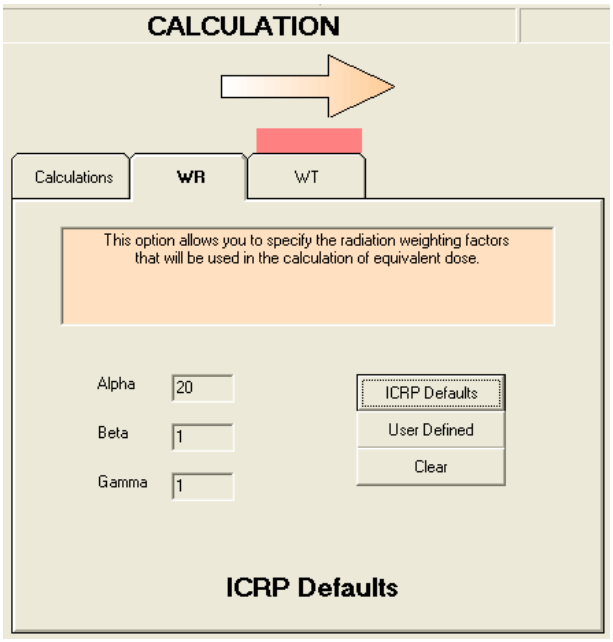


Figure 5.12. Selection of **ICRP-recommended Radiation Weighting Factors**.

Click the "**WR**" *tab* and *click* the "**ICRP Defaults**" button to load the *ICRP-recommended* values for the **Radiation Weighting Factors**. You can also define your own (**User Defined**) value for **Alpha**, **Beta** and/or **Gamma** radiation.

5.6.3. Selecting the Tissue Weighting Factors

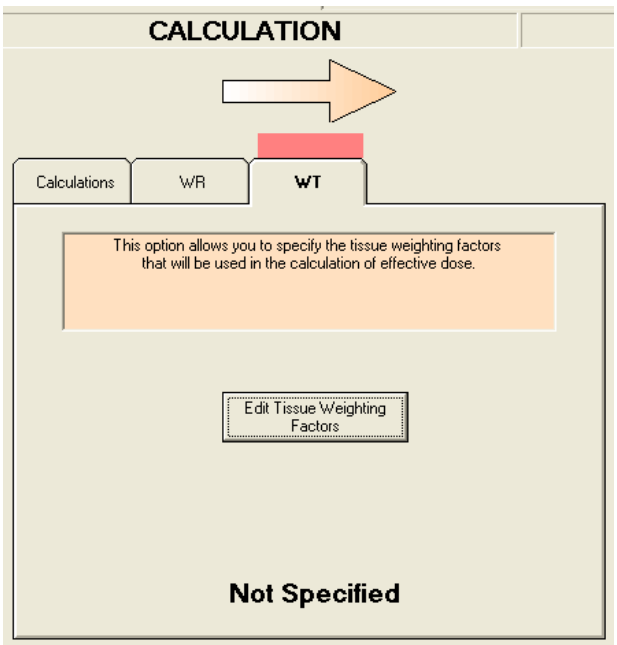

CALCULATION
Calculations
WR
WT
This option allows you to specify the tissue weighting factors that will be used in the calculation of effective dose.
Edit Tissue Weighting Factors
Not Specified

Figure 5.13. *Editing* (or *Selecting*) the **Tissue Weighting Factors** and **Remainder Tissue Rules**.

Click the "**WT**" *tab* to *select* or *edit* the **Tissue Weighting Factors** and **Remainder Tissue Rules** to be used for the calculation of **Effective Dose** (Figure 5.13). *Click* the "**Edit Tissue Weighting Factors**" button to view these selection options. Figure 5.14 shows selection of the 10 CFR 835 recommended weighting factors.

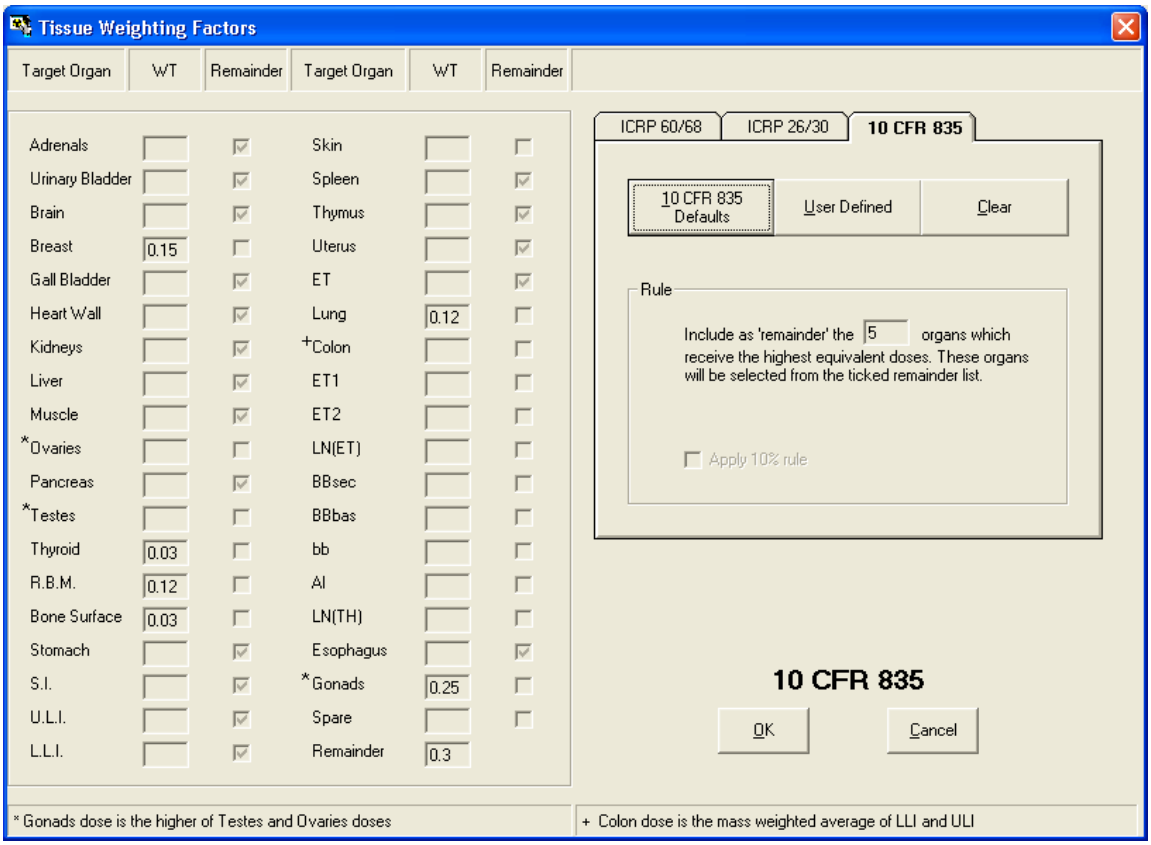


Figure 5.14. The **Tissue Weighting Factors** window.

In this window, you can also *opt* to use the values of **Tissue Weighting Factor** and **Remainder Tissue Rules** recommended in ICRP60, or those recommended in *ICRP26/30*, on which the **10 CFR 835** values are based.

5.7. Advanced Dose Calculation Menu

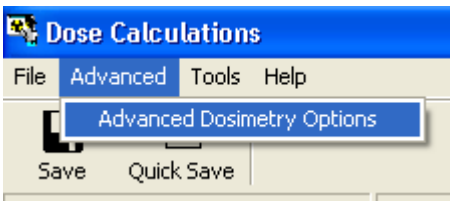


Figure 5.15. Tool to open the "**Advanced Dosimetry Options**" window.

The "**Advanced Dosimetry Options**" window gives the following options:

- "**Dose**" options - **Exclude nuclear recoil energy** from the SEEs for alpha emissions and/or **optimize calculation** speed for some radioactive progeny.
- "**Fitting**" options - Use **Least Squares** method, **Maximum Likelihood** method (default) or **Bayesian Analysis** in the bioassay fitting procedure.

- "**Bioassay**" option - Use measurements of **Am-241 activity in lungs** to evaluate Pu-241 content.
- "**Intake**" option - Specify **Intake** as **Mass** (in mg).

5.7.1. Nuclear Recoil Energy in SEE and 'Speed' Calculations

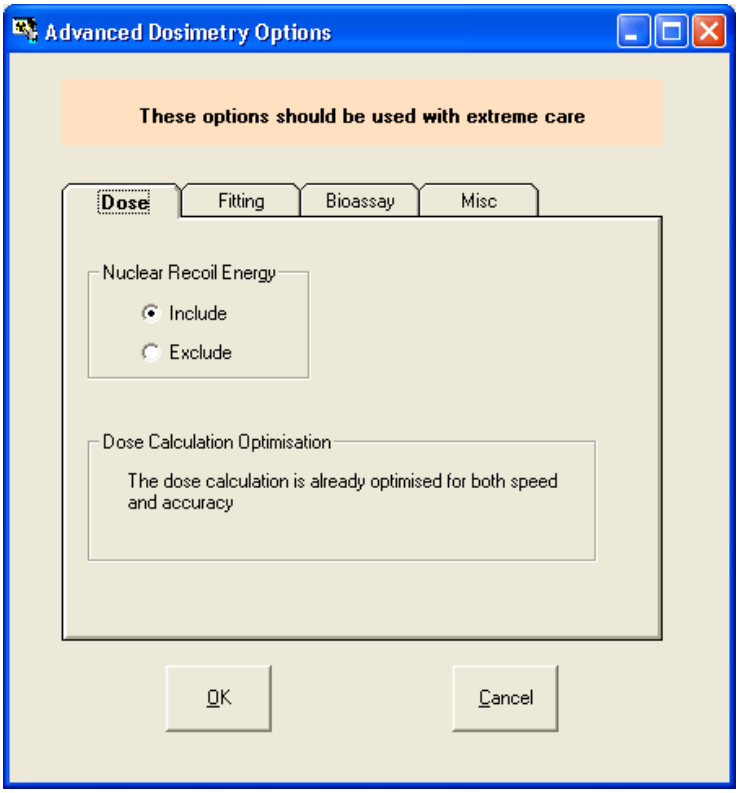


Figure 5.16. "**Dose**" **Options** window - showing option to **Exclude nuclear recoil energy** from the **SEEs** for alpha emissions.

By default, nuclear recoil energy is **included** in the SEEs for alpha emissions.

The "**Dose**" **Option** window (Figure 5.16) also displays the current status of "**Dose Calculation Optimization**". A choice to optimize the dose calculation for "**Speed**" or "**Accuracy**" appears automatically when this is necessary. The "choice" is necessary only for some cases involving intake of an indicator nuclide with radioactive progeny - see Appendix A: Accuracy of 'Speed' Option for applicability of this option. The "**Speed**" option is useful when accurate dose calculations can be carried out without having to calculate *explicitly* the *in-growth* of the radioactive progeny over time.

5.7.2. Fitting Options

Select to apply the "**Least Squares**", "**Maximum Likelihood**" (the default), or "**Bayesian**" fitting method (Figure 5.17) in the calculation of intake(s). This option is also available from the **Bioassay Calculations** screen (**Advanced Menu**).

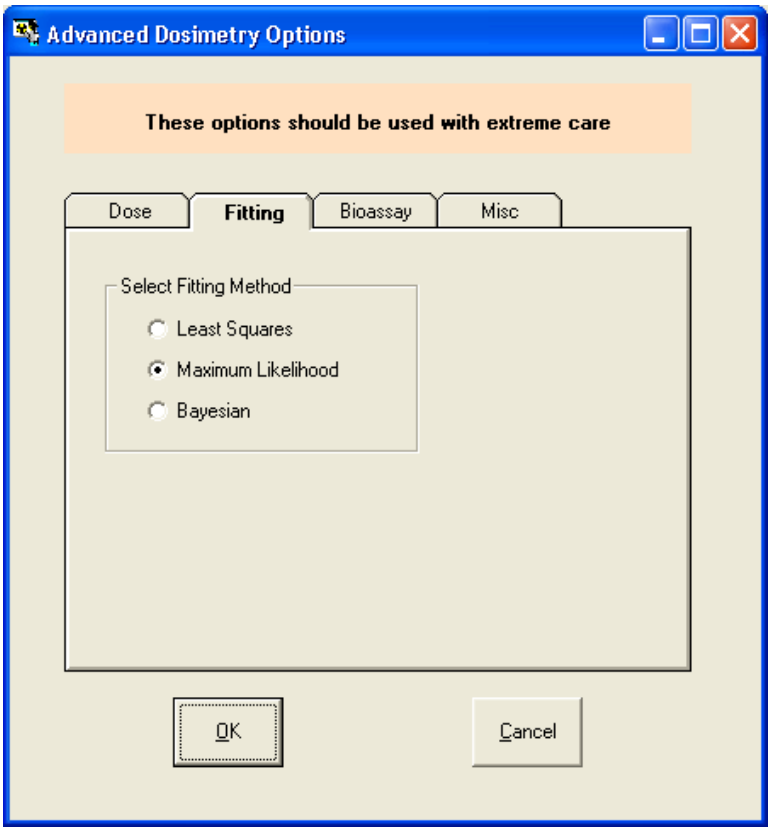


Figure 5.17. "Fitting" Options window.

5.7.3. Bioassay Option – Am-241 in Lungs

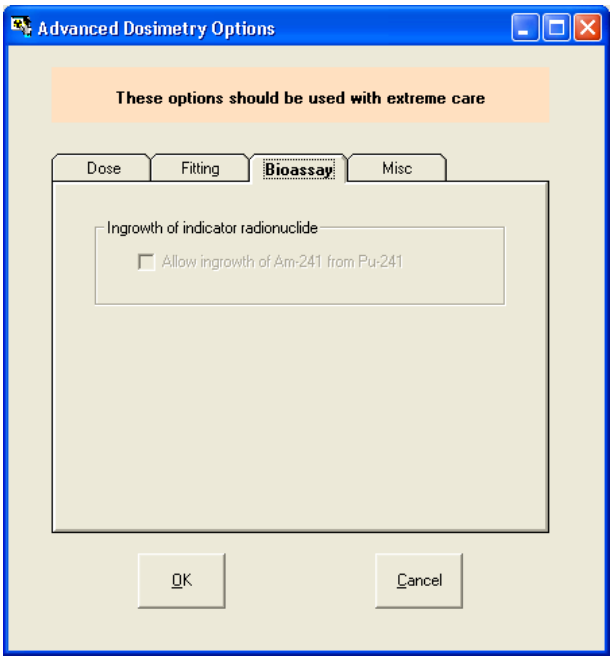


Figure 5.18. "Bioassay" Option window.

This option (Figure 5.18) enables measurements of ^{241}**Am**, *e.g.*, in the lungs, to be used as an indicator of ^{241}**Pu** activity, by automatically accounting for ^{241}**Am** in-growth over time (in the matrix of retained particles). The option is made available *automatically* when the **Indicator Nuclide** is defined as ^{241}**Am**, *AND* ^{241}**Pu** is included in the list of **Associated Radionuclides**. See **Appendix D: Example Bioassay Cases - "Case of Am-241 Lung Counting (for Pu-241)"** as an example.

5.7.4. Specify Intakes in Mass Units (mg)

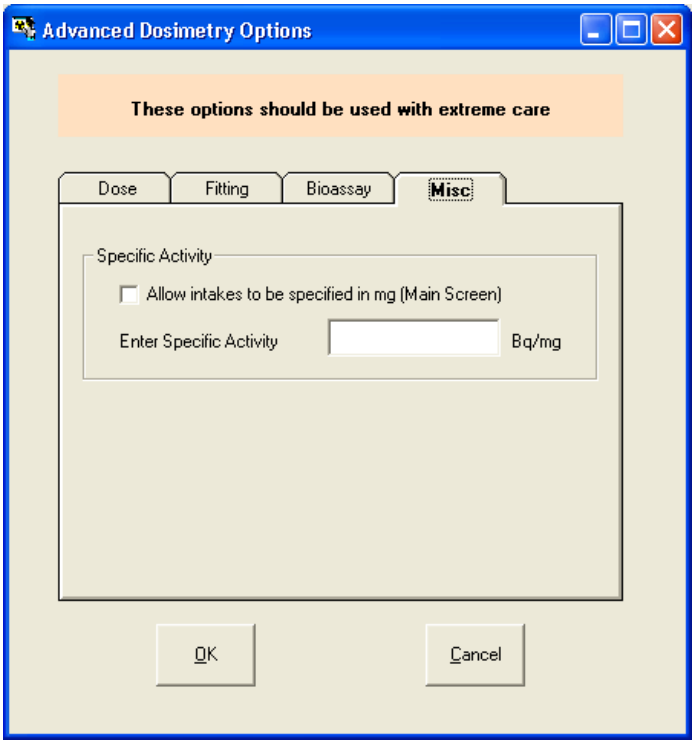


Figure 5.19. "Miscellaneous" Option - Use of **"Mass"** as the **Unit of Intake**.

When *checked*, this option allows **Intakes** to be specified in terms of **Mass** rather than **Activity**, with the associated **Specific Activity**. If you don't define the specific activity, you will be prompted to do this (figure 5.20).

Figure 5.20. Prompt to define **Specific Activity** in order to use **Mass** as the **Unit of Intake**.

Checking this option automatically highlights and enables the "**mg**" *Unit of Intake* in the "**Units**" panel of the **Main Screen** (Figure 5.21).

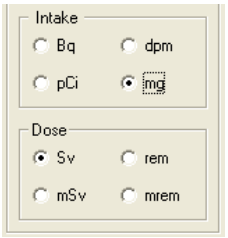


Figure 5.21. "**mg**" **Unit of Intake** enabled.

For an example of the use of "**Mass**" as the **Unit of Intake**, see **Appendix D: Example Bioassay Cases - "Case of Uranium Isotopic Mixture"**.

6. Example Committed Dose Calculation

	Note #1: This example illustrates the calculation of doses for the **multiple intakes** case (Miller et al., 1999) described in **Appendix D: Example Bioassay Cases "Estimating Multiple Intakes"** – Section D.3.).
	Note #2: the calculations performed here (directly in the **Dose Calculations** screen) are for **committed dose**, as needed for regulatory purposes, *e.g.*, to meet the requirements of **10 CFR 835**. The special calculations of annual dose received by designated target organs **required by NIOSH** (for application to **EEOICPA**) – which are accessed via the **Dose Calculations | Tools** menu – are described later (in Section 8).

Clicking the "**Dose Calculations**" button in the **Main Screen**, opens the **Dose Calculations** screen (Figure 6.1). The **Indicator Nuclide** defined in the Main Screen is automatically shown in the "**Dose from indicator radionuclide**" label - under the "**Calculations**" tab, in this example "**Pu-238**". Also, the previously estimated amounts of each intake (in this example **IR1**, **IR2** and **IR3**) are also displayed automatically under "**INTAKE**".

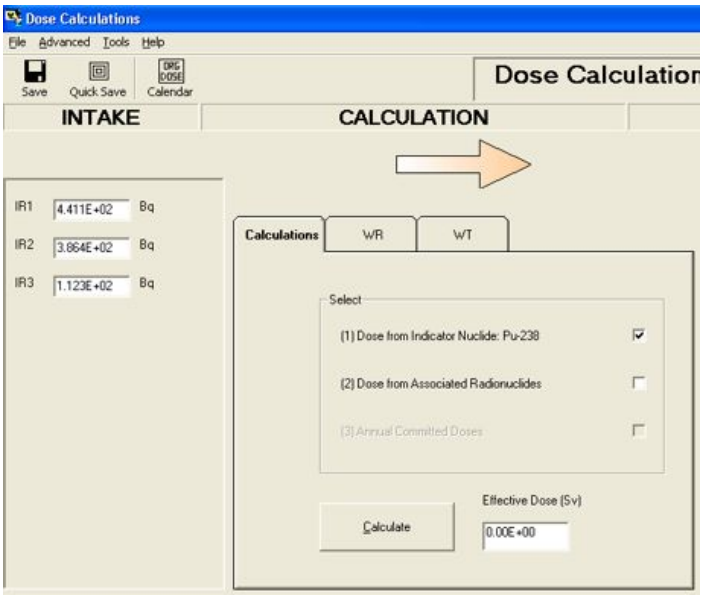


Figure 6.1. Checking the "**Dose from indicator radionuclide (Pu-238)**" dialog box in the **Dose Calculations** screen.

BEFORE *calculating* any doses, you need to *select* the values of **Radiation Weighting Factor** (w_R) to be used. This is done by *clicking* the "**WR**" tab in the "**CALCULATION**" sub-panel. If the values of w_R have NOT already been specified, the "**WR**" tab will appear as in Figure 6.2.

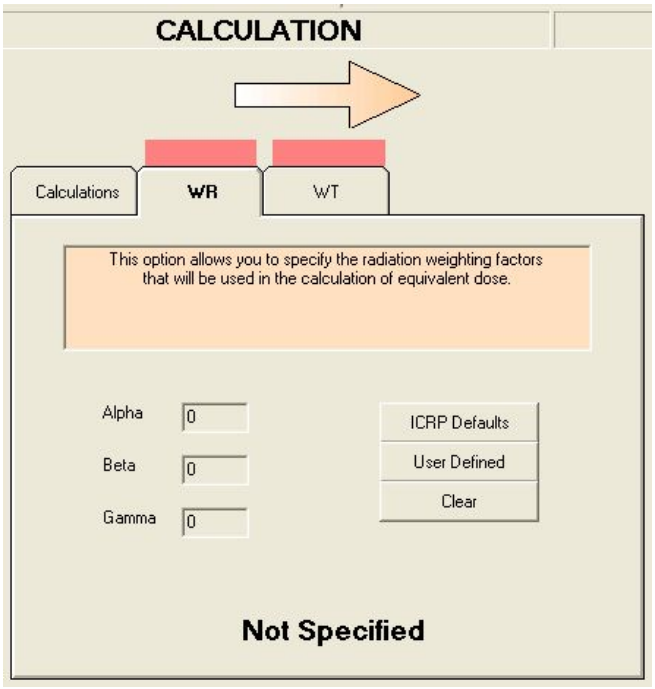


Figure 6.2. "**WR**" tab before values of the radiation weighting factor have been defined.

Click the "**ICRP Defaults**" button, to load the **ICRP-recommended** (as also prescribed by **10-CFR-835**) values of w_R:

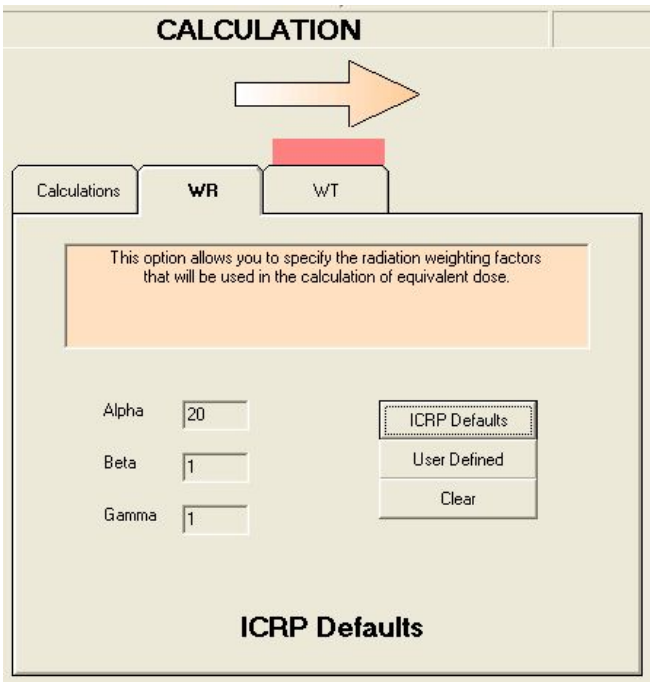


Figure 6.3. Loading the **ICRP Default** values of radiation weighting factor.

Click the "**WT**" tab to *select* the **tissue weighting factors** (w_T) - see Figure 6.4.

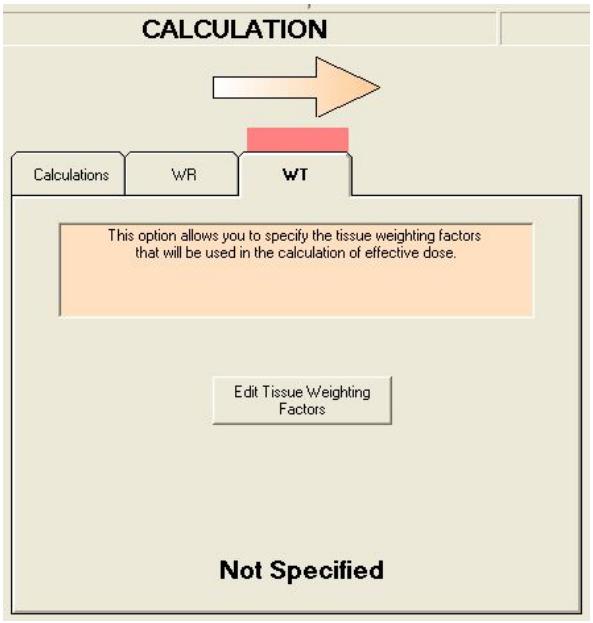

CALCULATION
Calculations
WR
WT
This option allows you to specify the tissue weighting factors that will be used in the calculation of effective dose.
Edit Tissue Weighting Factors
Not Specified

Figure 6.4. Selection of tissue weighting factors.

Click the "**Edit Tissue Weighting Factors**" button to *select* and/or *confirm* the **CFR 835** prescribed values of tissue weighting factors and the **remainder tissue rules** (Figure 6.5). *Click* the "**OK**" button to *apply* these values – and *return* to the **Dose Calculations** screen.

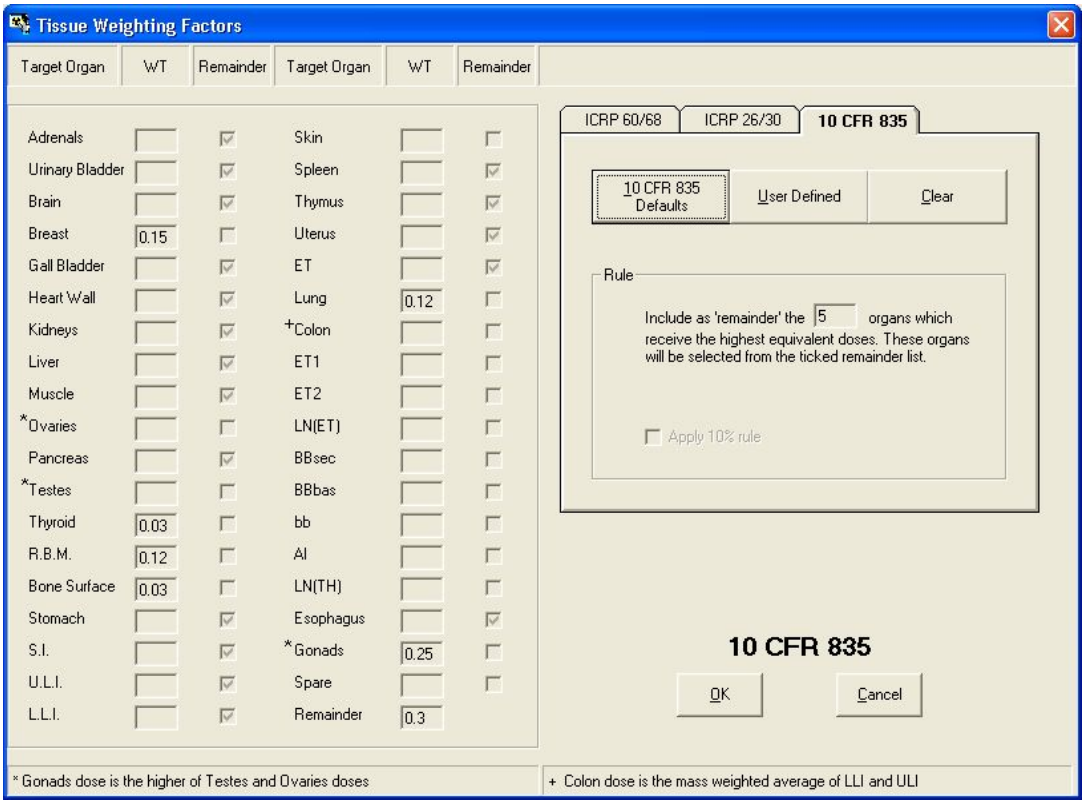


Figure 6.5. Selection of **10 CFR 835** values for the tissue weighting factors and remainder tissue rules.

6.1. Calculation of Equivalent Doses

To *calculate* the **equivalent doses** committed to **target tissues** (from **each of the 3 intakes**):

- *click* the "**Calculations**" *tab*;
- *click* the "**Calculate**" *button*.

The **calculated doses** will be displayed in the "**DOSE**" table for the **Indicator Radionuclide** (Figure 6.6). Use the *scroll bar* (right-side) to *view* the **equivalent doses** calculated for the additional **Target Organs**.

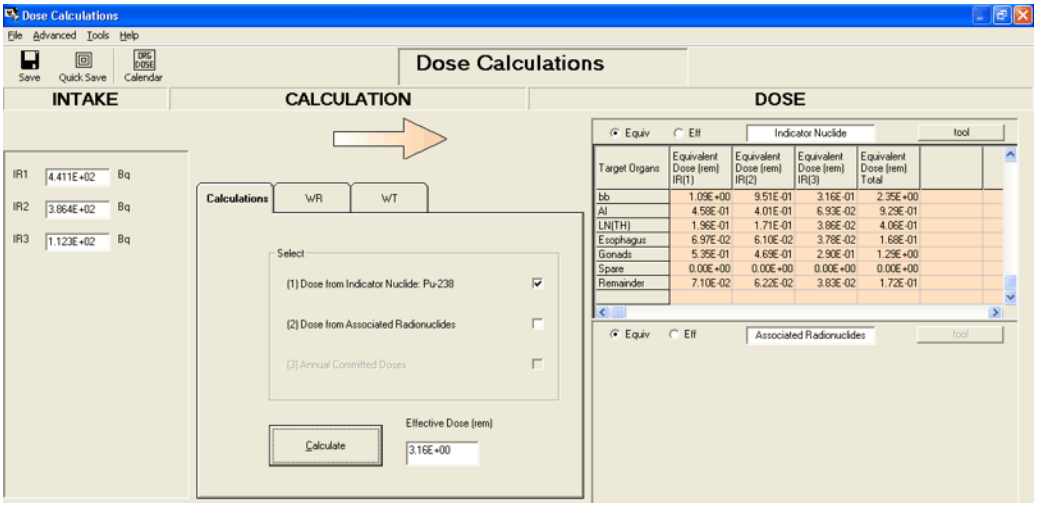


Figure 6.6. Calculated values of **Equivalent Dose** (for the **Indicator Radionuclide**).

6.2. Display of Effective Doses

IMBA Expert™ OCAS/ORAU-Edition calculates (and **stores**) ALL doses of interest (including the **effective dose resulting from each intake**) in one step. Therefore, it is not necessary to carry out a further calculation to **display the effective doses**. Simply *click* the "**Eff**" *option* to *switch* the display to **Effective Dose** (Figure 6.7).

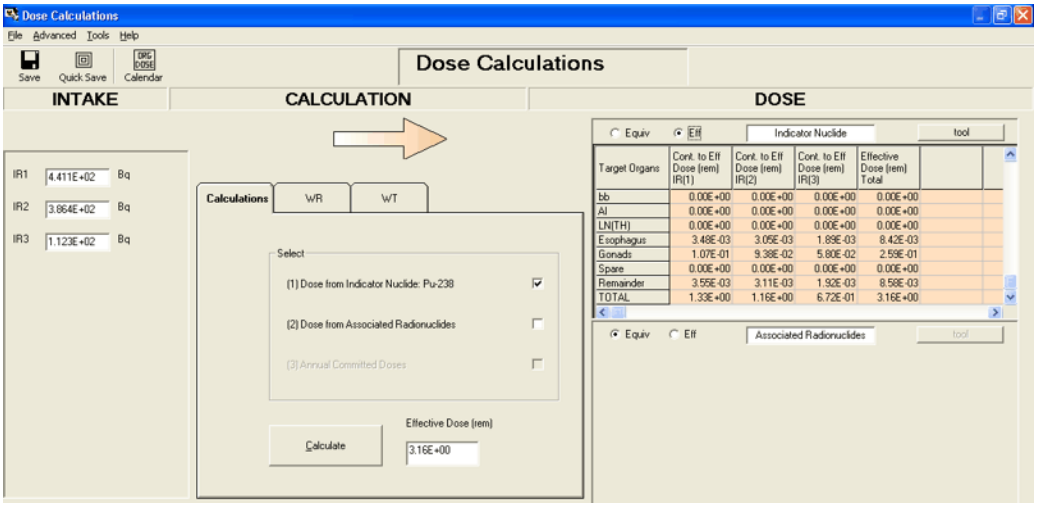
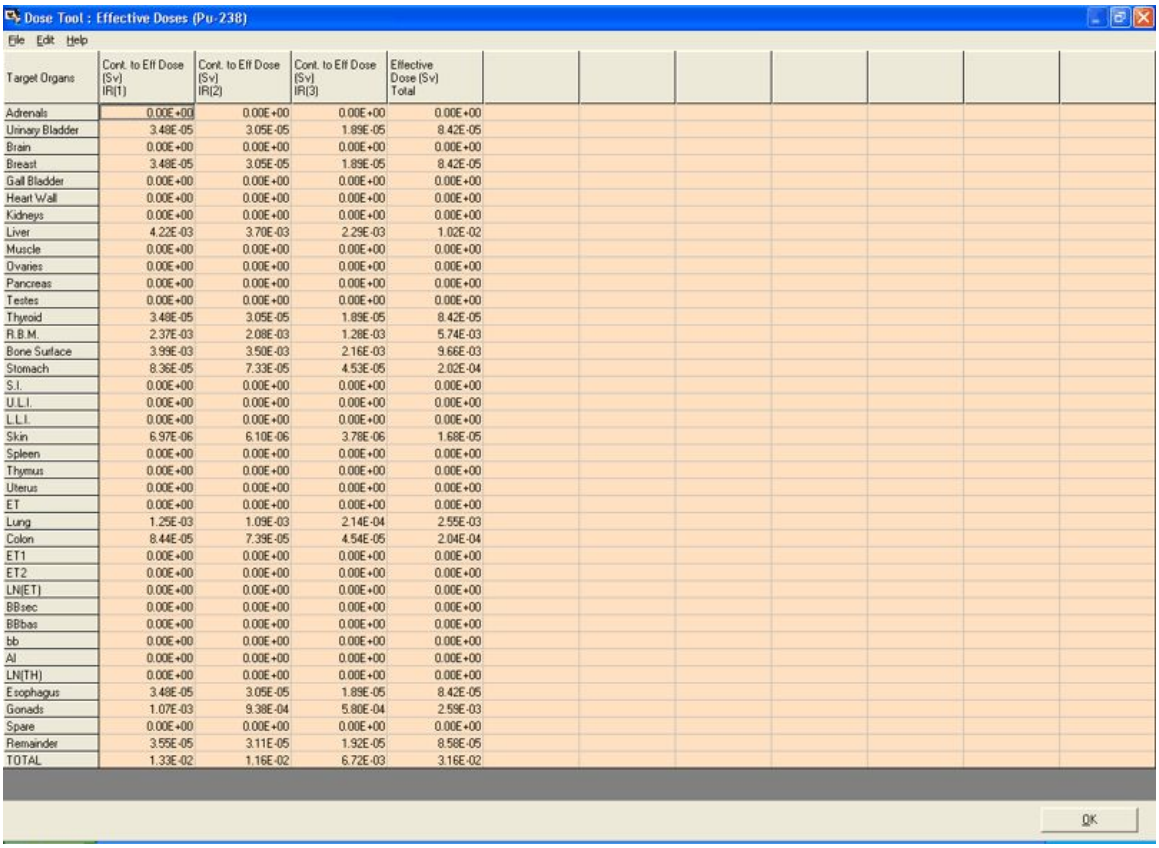


Figure 6.7. Displaying the **TOTAL Effective Dose** resulting from **each intake** (and the contributions from each target organ).

Clicking the "**tool**" button (top-right-corner of the "**Indicator Nuclide**" dose results window) displays an expanded table of results (Figure 6.8).



Target Organs	Cont. to Eff Dose (Sv) IR(1)	Cont. to Eff Dose (Sv) IR(2)	Cont. to Eff Dose (Sv) IR(3)	Effective Dose (Sv) Total
Adrenals	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Urinary Bladder	3.48E-05	3.05E-05	1.89E-05	8.42E-05
Brain	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Breast	3.48E-05	3.05E-05	1.89E-05	8.42E-05
Gall Bladder	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Heart Wall	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Kidneys	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Liver	4.22E-03	3.70E-03	2.29E-03	1.02E-02
Muscle	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Ovaries	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Pancreas	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Testes	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Thyroid	3.48E-05	3.05E-05	1.89E-05	8.42E-05
R.B.M.	2.37E-03	2.08E-03	1.28E-03	5.74E-03
Bone Surface	3.99E-03	3.50E-03	2.16E-03	9.66E-03
Stomach	8.36E-05	7.33E-05	4.53E-05	2.02E-04
S.I.	0.00E+00	0.00E+00	0.00E+00	0.00E+00
U.L.I.	0.00E+00	0.00E+00	0.00E+00	0.00E+00
L.L.I.	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Skin	6.97E-06	6.10E-06	3.78E-06	1.68E-05
Spleen	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Thymus	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Uterus	0.00E+00	0.00E+00	0.00E+00	0.00E+00
ET	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Lung	1.25E-03	1.09E-03	2.14E-04	2.55E-03
Colon	8.44E-05	7.39E-05	4.54E-05	2.04E-04
ET1	0.00E+00	0.00E+00	0.00E+00	0.00E+00
ET2	0.00E+00	0.00E+00	0.00E+00	0.00E+00
LN(ET)	0.00E+00	0.00E+00	0.00E+00	0.00E+00
BBsec	0.00E+00	0.00E+00	0.00E+00	0.00E+00
BBbas	0.00E+00	0.00E+00	0.00E+00	0.00E+00
bb	0.00E+00	0.00E+00	0.00E+00	0.00E+00
AI	0.00E+00	0.00E+00	0.00E+00	0.00E+00
LN(TH)	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Esophagus	3.48E-05	3.05E-05	1.89E-05	8.42E-05
Gonads	1.07E-03	9.38E-04	5.80E-04	2.59E-03
Spare	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Remainder	3.55E-05	3.11E-05	1.92E-05	8.58E-05
TOTAL	1.33E-02	1.16E-02	6.72E-03	3.16E-02

Figure 6.8. Expanded view of the organ contributions to effective dose for each **Intake** of the **Indicator Nuclide**.

The values of **Effective Dose** that are calculated to result from **each separate intake** of the **Indicator Nuclide** (in the **multiple intakes** example case) are:

- E_{IR1} **= 13.3 mSv** (1.3 rem);
- E_{IR2} **= 11.6 mSv** (1.2 rem);
- E_{IR3} **= 6.7 mSv** (0.7 rem).

The **TOTAL Effective Dose** (from **all Intakes**) is calculated to be **31.6 mSv** (3.2 rem).

Tip: It is instructive to repeat the above calculation for the "initial" and each subsequent estimate of the intake amounts (see **Appendix D: Example Bioassay Cases**, Section D.3.13. – "**Optimizing the Intake Estimation**"), together with their respective assumed **Model Parameters**. This will indicate the **range of uncertainty** in the calculated **Effective Dose** that results solely from the **intake estimation process**. Try this for yourself – it is quick and easy! Uncertainties in the biokinetic models (and dose-weighting factors) will, of course, contribute **additional uncertainty** to the **Effective Dose**.

Tip: Also try repeating the example dose calculation after selecting **ICRP60/68** tissue weighting factors and remainder tissue rules.

6.3. Calculating Doses from Associated Radionuclides

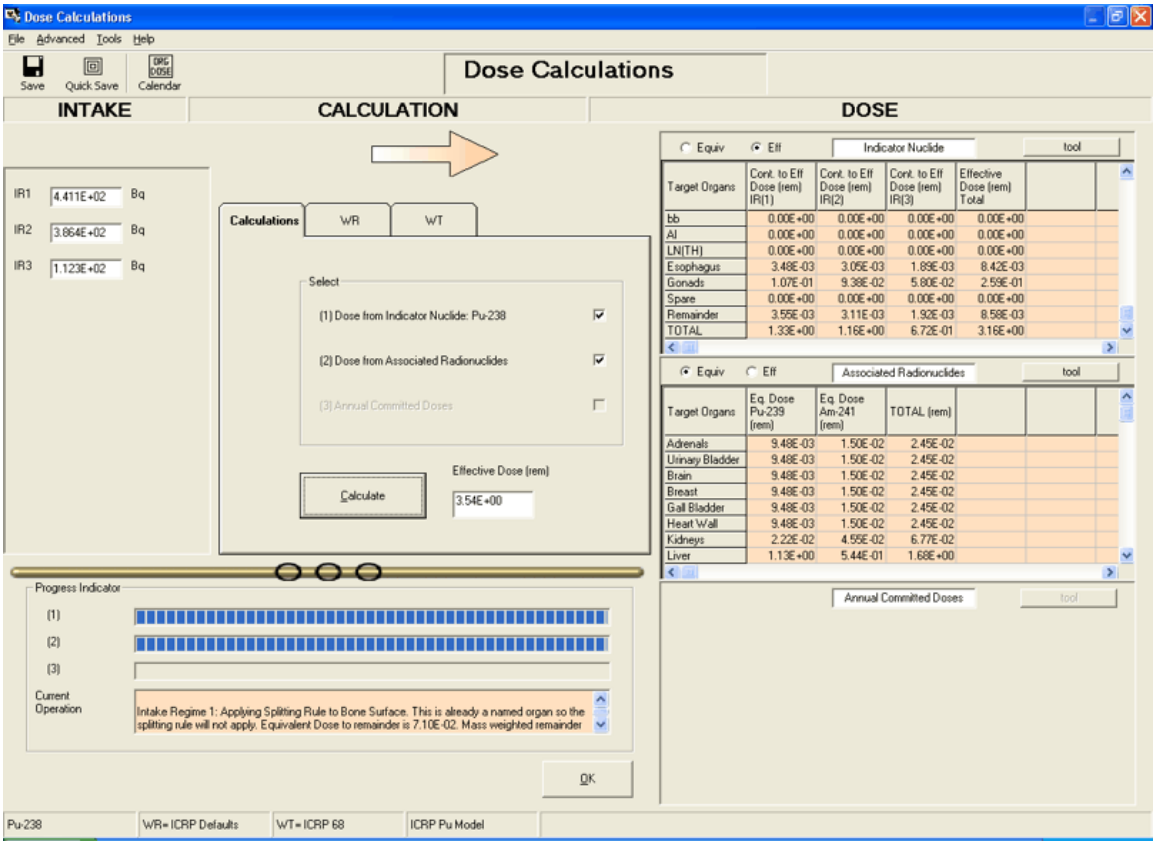


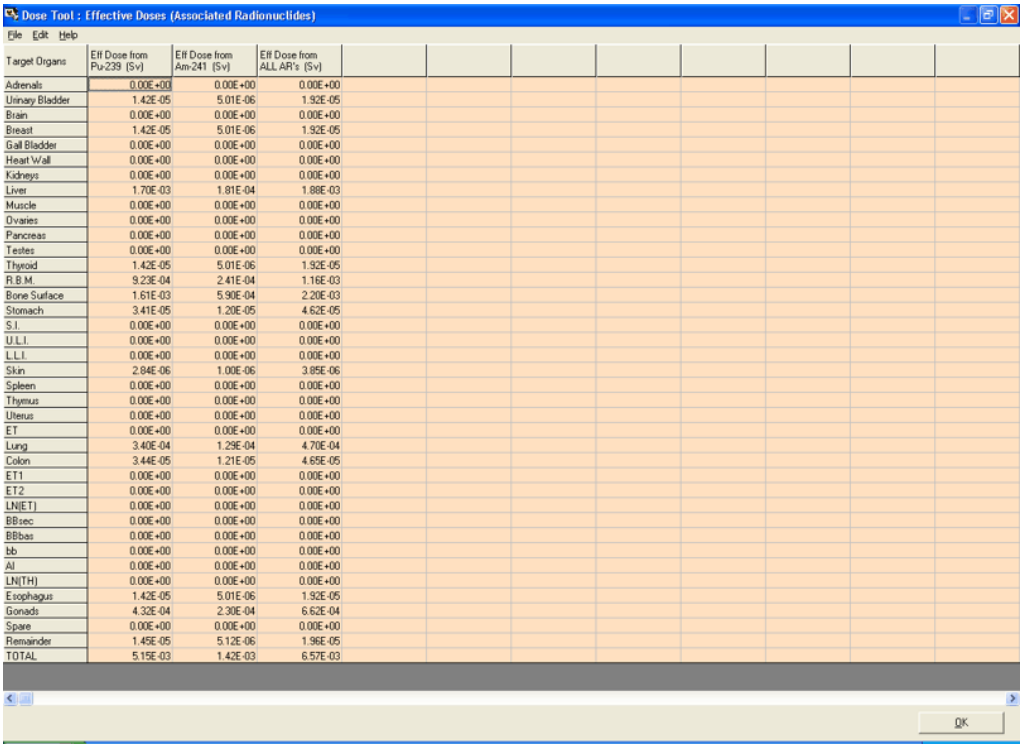
Figure 6.9. Calculating and displaying doses from **Associated Radionuclides**.

Doses from **Associated Radionuclides** are calculated at the same time as those from the **Indicator Nuclide** – see Section 5.7., "**Dose Results Windows**". In fact, setting up the dose calculation for **Associated Radionuclides** is even simpler than setting up the **Indicator Radionuclide** dose calculation:

1. *Select* each **Associated Radionuclide** - from the **Periodic Table of the Elements** (in the **Main Screen**).
2. *Define* the **Abundance** (in %) of each **Associated Radionuclide** relative to the activity of the **Indicator Nuclide** - this is assumed to be the same for **all Intake Regimes**.
3. *Check* the "**Dose from Associated Radionuclides**" box in the "**Calculations**" sub-panel (**Dose Calculations** screen).
4. *Click* the "**Calculate**" *button*.

IMBA Expert™ OCAS/ORAU-Edition will automatically load the recommended **ICRP Biokinetic Model** for each **Associated Radionuclide** (to calculate the number of disintegrations in each Source Organ) and then use the recommended **ICRP SEE Data File** to calculate the resulting doses to Target Organs. See also **Appendix A: Technical Basis**, Section A.9.2.2. – "**CED from Associated Radionuclides**".

Clicking the "**tool**" button (top-right-corner of the "**Indicator Nuclide**" dose results window) displays an expanded table of results (Figure 6.10).



Target Organs	Eff Dose from Pu-239 (Sv)	Eff Dose from Am-241 (Sv)	Eff Dose from ALL AR's (Sv)
Adrenals	0.00E+00	0.00E+00	0.00E+00
Urinary Bladder	1.42E-05	5.01E-06	1.92E-05
Brain	0.00E+00	0.00E+00	0.00E+00
Breast	1.42E-05	5.01E-06	1.92E-05
Gall Bladder	0.00E+00	0.00E+00	0.00E+00
Heart Wall	0.00E+00	0.00E+00	0.00E+00
Kidneys	0.00E+00	0.00E+00	0.00E+00
Liver	1.70E-03	1.81E-04	1.88E-03
Muscle	0.00E+00	0.00E+00	0.00E+00
Ovaries	0.00E+00	0.00E+00	0.00E+00
Pancreas	0.00E+00	0.00E+00	0.00E+00
Testes	0.00E+00	0.00E+00	0.00E+00
Thyroid	1.42E-05	5.01E-06	1.92E-05
R.B.M.	9.23E-04	2.41E-04	1.16E-03
Bone Surface	1.61E-03	5.90E-04	2.20E-03
Stomach	3.41E-05	1.20E-05	4.62E-05
S.I.	0.00E+00	0.00E+00	0.00E+00
U.L.I.	0.00E+00	0.00E+00	0.00E+00
L.L.I.	0.00E+00	0.00E+00	0.00E+00
Skin	2.84E-06	1.00E-06	3.85E-06
Spleen	0.00E+00	0.00E+00	0.00E+00
Thymus	0.00E+00	0.00E+00	0.00E+00
Uterus	0.00E+00	0.00E+00	0.00E+00
ET	0.00E+00	0.00E+00	0.00E+00
Lung	3.40E-04	1.29E-04	4.70E-04
Colon	3.44E-05	1.21E-05	4.65E-05
ET1	0.00E+00	0.00E+00	0.00E+00
ET2	0.00E+00	0.00E+00	0.00E+00
LN(ET)	0.00E+00	0.00E+00	0.00E+00
BBsec	0.00E+00	0.00E+00	0.00E+00
BBbas	0.00E+00	0.00E+00	0.00E+00
bb	0.00E+00	0.00E+00	0.00E+00
AI	0.00E+00	0.00E+00	0.00E+00
LN(TH)	0.00E+00	0.00E+00	0.00E+00
Esophagus	1.42E-05	5.01E-06	1.92E-05
Gonads	4.32E-04	2.30E-04	6.62E-04
Spare	0.00E+00	0.00E+00	0.00E+00
Remainder	1.45E-05	5.12E-06	1.96E-05
TOTAL	5.15E-03	1.42E-03	6.57E-03

Figure 6.10. Expanded view of the organ contributions to effective dose for the **Indicator Nuclide** and all **Associated Radionuclides**.

7. Producing a Case Report

To *generate* a **Report** of your complete case analysis, *click* the "**Report**" *tool* (second row of the **Main Screen**). This will *open* the **Report** window (Figure 7.1).

Note: IMBA Expert™ OCAS/ORAU-Edition includes a **special report tool** that automatically includes in the report **claimant information** and **calculated annual doses to a selected target organ** - in the precise format required for input to '**FeedIREP**'.

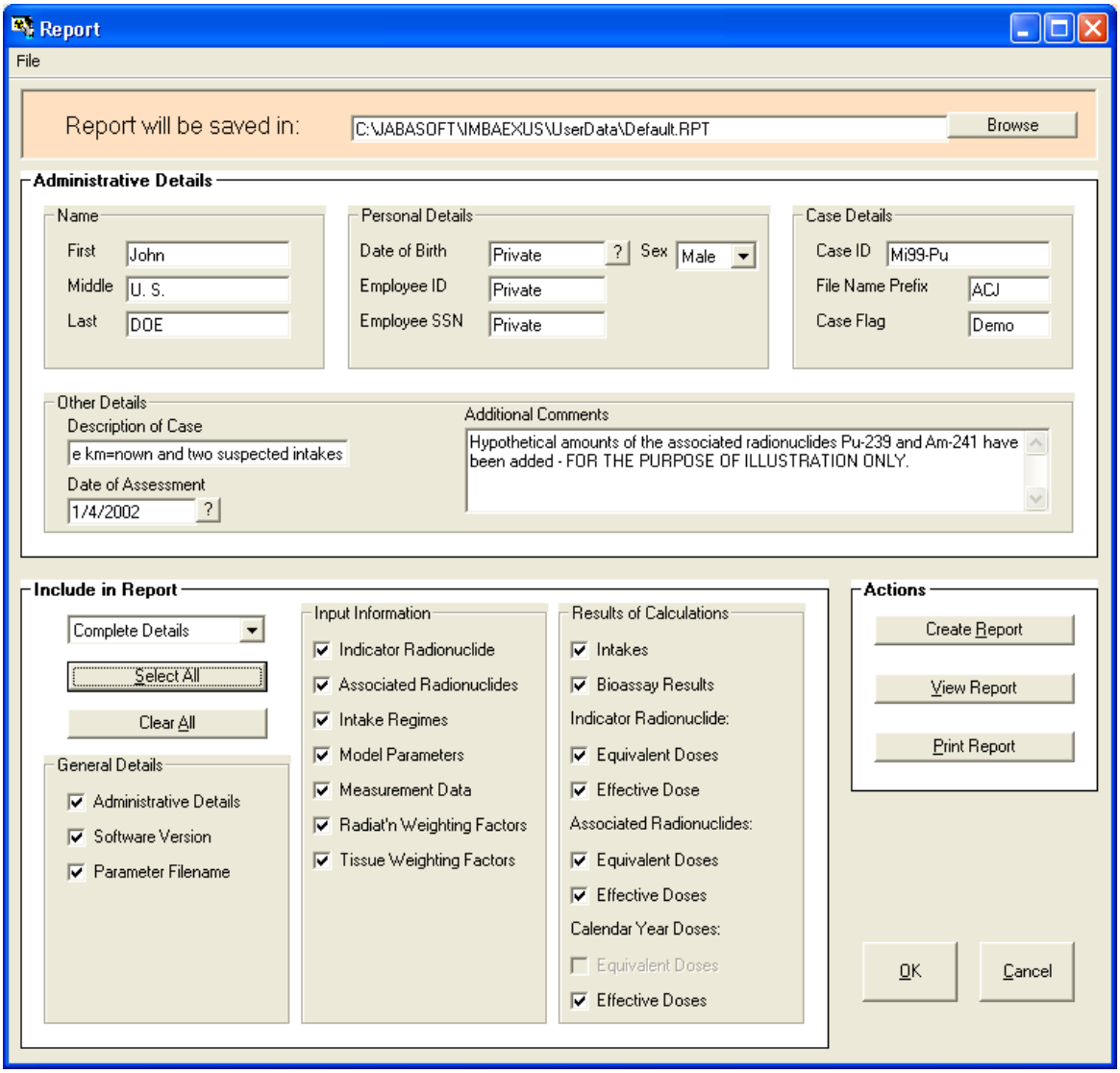


Figure 7.1. Report Generator (window) used to set up a comprehensive **Case Report**.

As shown in Figure 7.1, you can *check* the associated box to include **selected information** in your **Report** - or *click* the "**Select All**" button to specify a **fully comprehensive report**.

Tip: The **Report File** generated by *clicking* the "**Create Report**" *button* for the example **Report** settings shown in Figure 6.1 is *saved* (by default) in the **"[Install Drv]:\JABASOFT\IMBAEXUS\UserData\Demo\"** folder - or you can "**browse**" to save this in a different folder.

8. Special Applications for EEOICPA

IMBA Expert™ OCAS/ORAU-Edition is designed specifically to meet **NIOSH**'s requirements under the Energy Employees' Occupational Illness Compensation Program Act (EEOICPA 2000). In particular, the software is customized to do the following:

1. Provide all of the capabilities of the IMBA Expert™ USDOE-Edition (Phase II) software for analyzing bioassay data and estimating the most likely intake(s) of radionuclides, as described in the previous sections of this **User Manual**. The software is designed to provide the means for initial input of bioassay data – *via* the built-in **Table Tool** (Section 4.5) – for each individual claimant whose internal exposure is to be assessed.

2. Calculate equivalent doses received by specific target organs and tissues in each **Calendar Year** – from the start of a claimant's qualifying occupational exposure through to the date(s) of diagnosis of the claimant's qualifying cancer(s).

3. Import claimant-specific information in a standard format – from the '**Initiation file**' (***.ini**) generated by Oak Ridge Associated Universities Inc.'s (ORAU's) Energy Employees Occupational Illness Compensation Program Dose Reconstruction Project.

4. Interface with the **I**nteractive **R**adio**E**pidemiology **P**rogram (**NIOSH-IREP**) – for calculation of the probability distribution of cancer causation.

Important Note: IMBA Expert™ OCAS/ORAU-Edition is designed to function best in the above listed order – for each internal dose assessment, *i.e.*, **(1)** carry out the bioassay data analysis and assessment of intake(s), **then (2)** 'merge' the calculated annual equivalent doses with the externally generated claimant case data (in the form of a standard **Initiation file** – '***.ini**') – **in order to (3)** produce a complete case report suitable for **direct** input into '**FeedIREP**'.

8.1. Dose Calculations for NIOSH-IREP

We will use here the example bioassay data analysis for the IAEA (1999) whole-body activity measurements of ^{60}Co (Annex IV Case 3) to illustrate the calculation of annual equivalent doses to designated target organs in relation to a hypothetical diagnosis of cancer. Figure 8.1 shows the **Main Screen** of IMBA Expert™ OCAS/ORAU-Edition after opening the file **[Install Drv]:\\JABASOFT\IMBAEXUS\UserData1\Demo\IAEA Case 3 - 60Co.ix**.

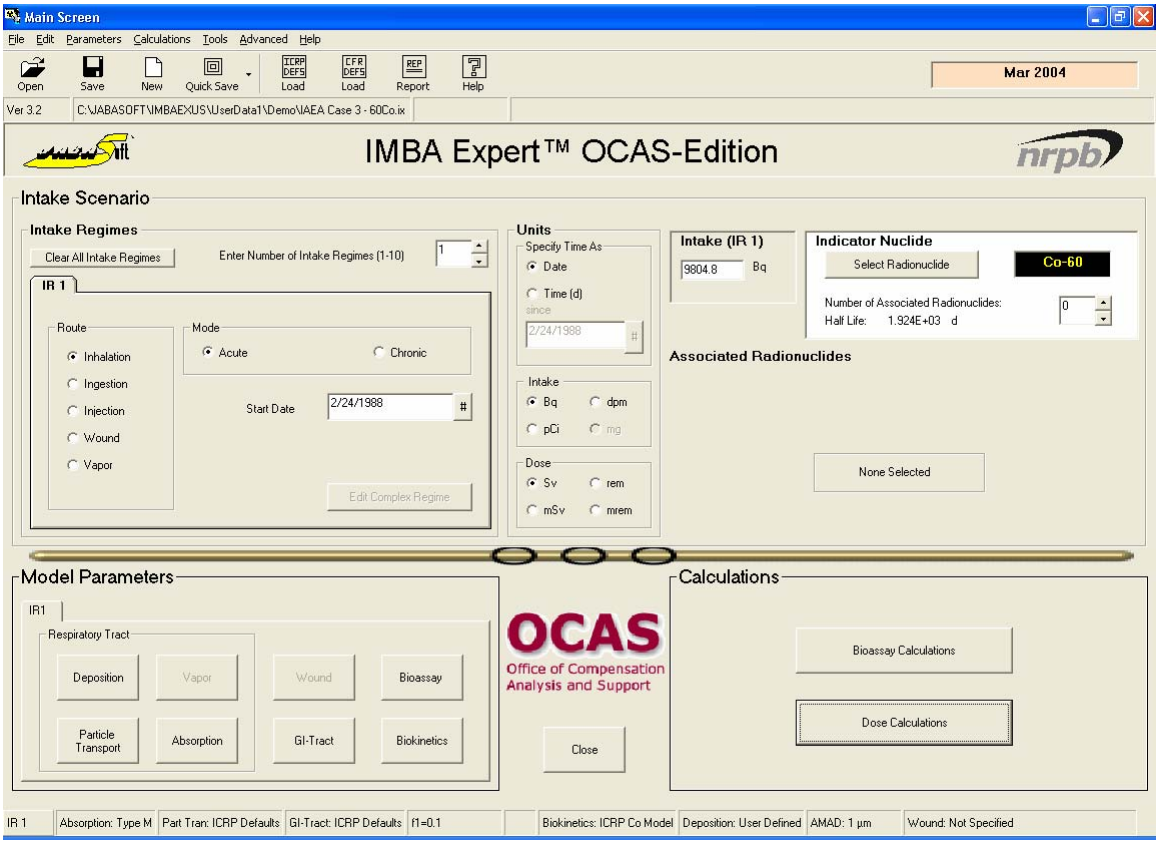


Figure 8.1. Main Screen after opening the parameter file "**IAEA Case 3 - 60Co.ix**.

Important Note: NIOSH-IREP requires calculated annual equivalent doses to be expressed in **centi-Sv** (**cSv**), *i.e.,* in the traditional dose unit '**rem**'. Therefore, it is IMPORTANT to ensure that you have selected 'rem' as the dose unit (in the **Main Screen**) - as shown in Figure 8.1.

In this example case, the most likely intake was calculated to be 9,805 Bq - by inhalation of a 1-µm AMAD aerosol of 'Type M' ^{60}Co on February 24th, 1988. To calculate the annual equivalent doses received by all target organs or tissues:

- *click* the "**Dose Calculations**" button - to open the **Dose Calculations** screen.
- click the "**ORG DOSE Calendar**" button - to open the **'Equivalent Dose to selected organ received in each calendar year'** window (Figure 8.2).

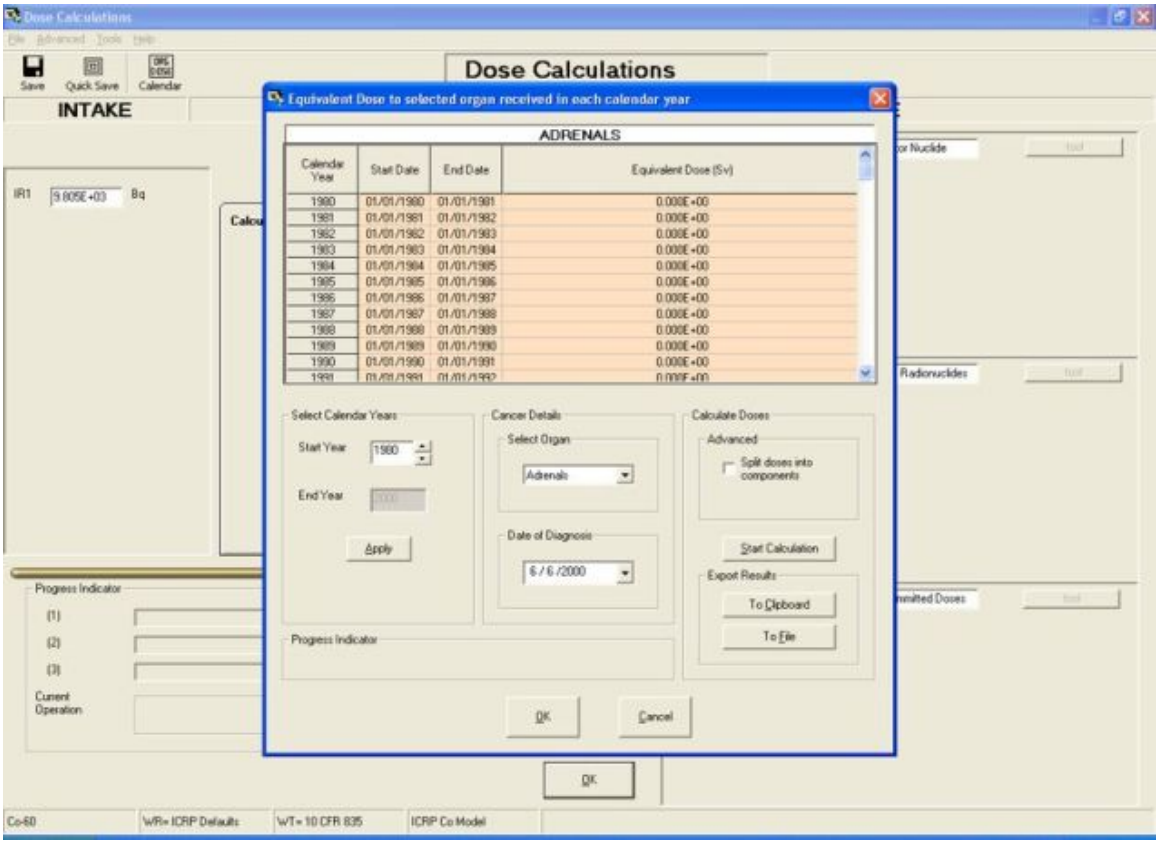


Figure 8.2. Opening the **'Equivalent Dose to selected organ received in each calendar year**' window.

	Note #1: The '**Equivalent Dose to selected organ received in each calendar year**' window opens with the default settings shown in Figure 8.2, *i.e.*, **'Start Year**' = 1980; '**Select Organ**' = Adrenals; '**Date of Diagnosis**' = 6/6/2000; '**Split doses into components**' = unchecked.
	Note #2: As specified by **NIOSH/OCAS**, Version 3.2 of IMBA Expert™ OCAS/ORAU-Edition enables you to select for display (and to send to the output report file) the calculated annual doses received by ONE designated target organ, as **selected** from a drop-down list. It is anticipated that a future enhanced version of the software will enable you to **select several** target organs (or tissues) for which the calculated annual doses will ALL be tabulated in the output report file. In Version 4.0, a separate output report file is needed to pass the calculated annual doses for each additional target organ (or tissue) to '**FeedIREP**'.
	Note #3: Again, as per initial specification, Version 3.2 of IMBA Expert™ OCAS/ORAU-Edition enables you to define a time-span of up to 50 years for calculation of the annual doses received by target organs. However, in practice, it has been found that greater time-spans may be needed in some cases. Accordingly, it is anticipated that a future enhance version of the software will enable annual doses for a time-span of up to 70 y to be calculated (in a single step).
	Note #4: The selected **'tissue weighting factors**' - shown in the '**Status Bar**' (Figure 8.2) do NOT affect the calculated values of **equivalent dose**. These apply ONLY to the calculation of **effective dose**.

8.1.1. Example Annual Dose Calculation

We will assume for this example (**IAEA Case 3 - 60Co.ix**):

- that the (hypothetical) claimant data file defines the diagnosed cancer as "**Cancer1=Stomach (151)**";

- that the (hypothetical) claimant data file defines the '**Date of Diagnosis**' as "**Cancer1DiagnosisDate=02/25/1997**".

The corresponding data values in the '**Equivalent Dose to selected organ received in each calendar year**' are shown in Figure 8.3.

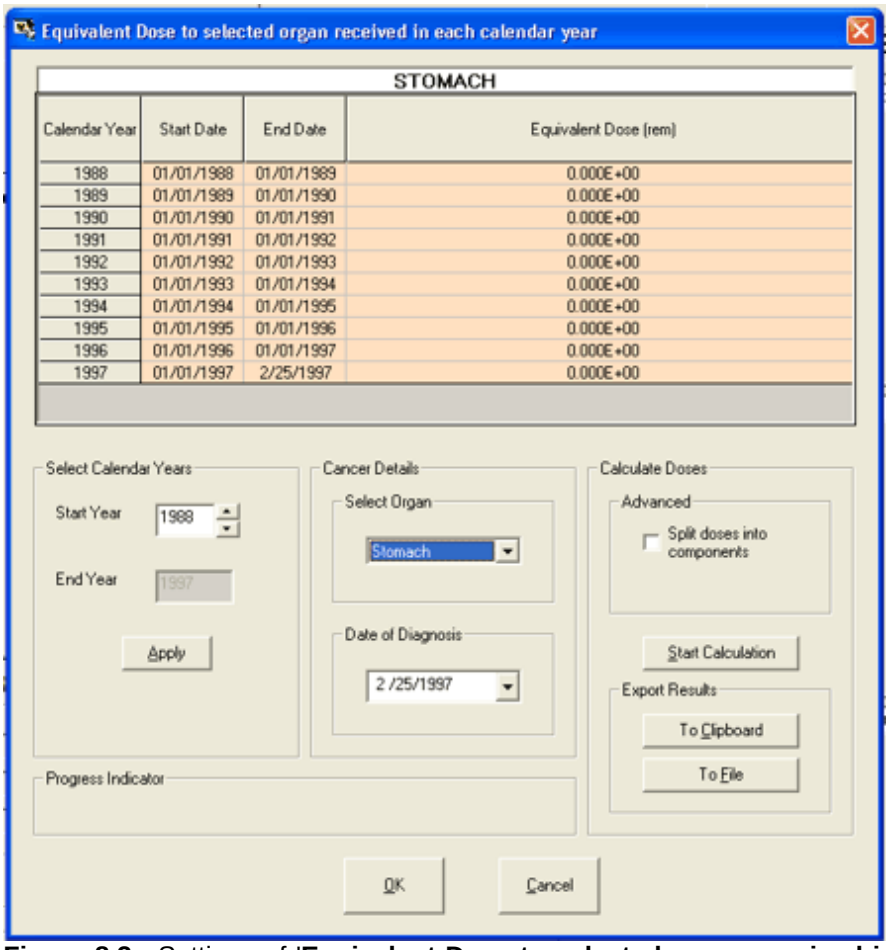


Figure 8.3. Settings of '**Equivalent Dose to selected organ received in each calendar year**' window for hypothetical case of stomach cancer.

To calculate the total annual equivalent doses, you simply *click* the '**Start Calculation**' button. The resulting values are shown (in '**rem**') in Figure 8.4.

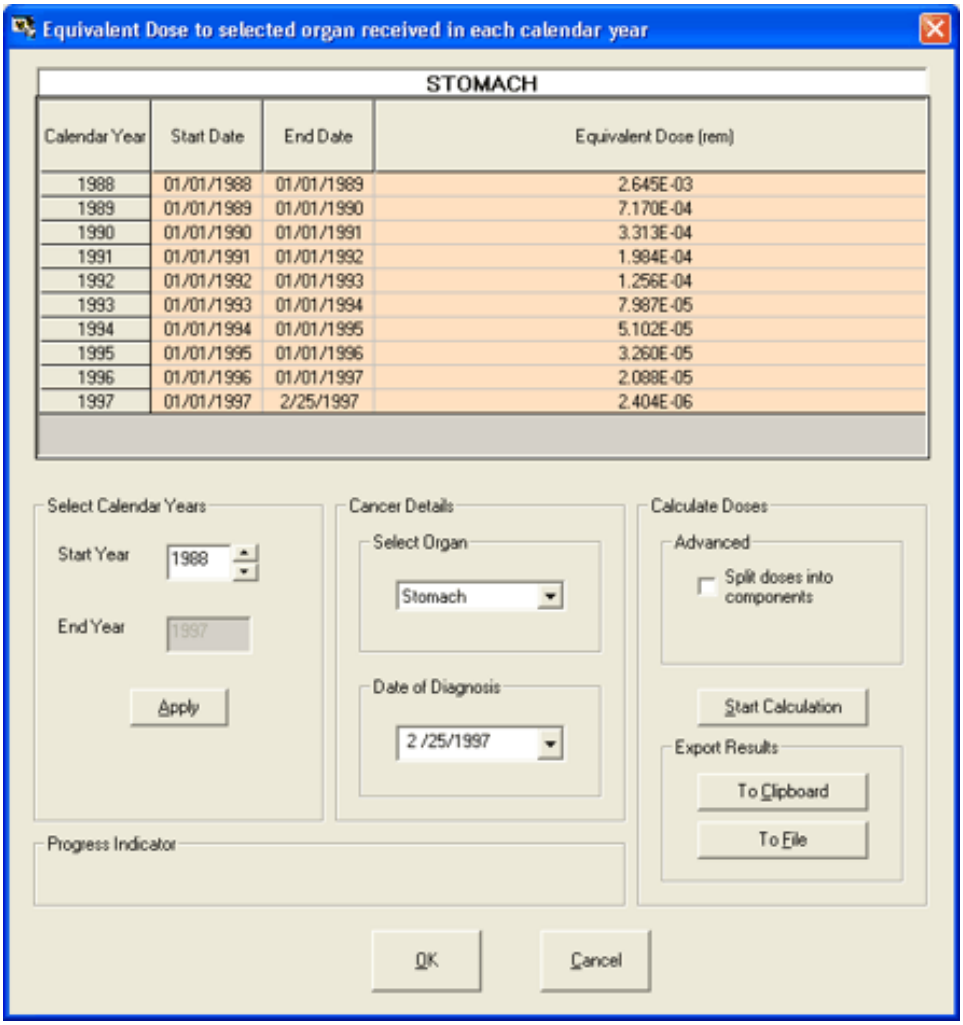


Figure 8.4. Total annual equivalent doses displayed for the stomach wall.

To '**split**' the annual equivalent doses into separate **alpha**, **beta**, and **gamma** components, you simply *check* the '**Split doses into components**' box before clicking the '**Start Calculation**' button. The resulting 'split' values are shown (in '**rem**') in Figure 8.5.

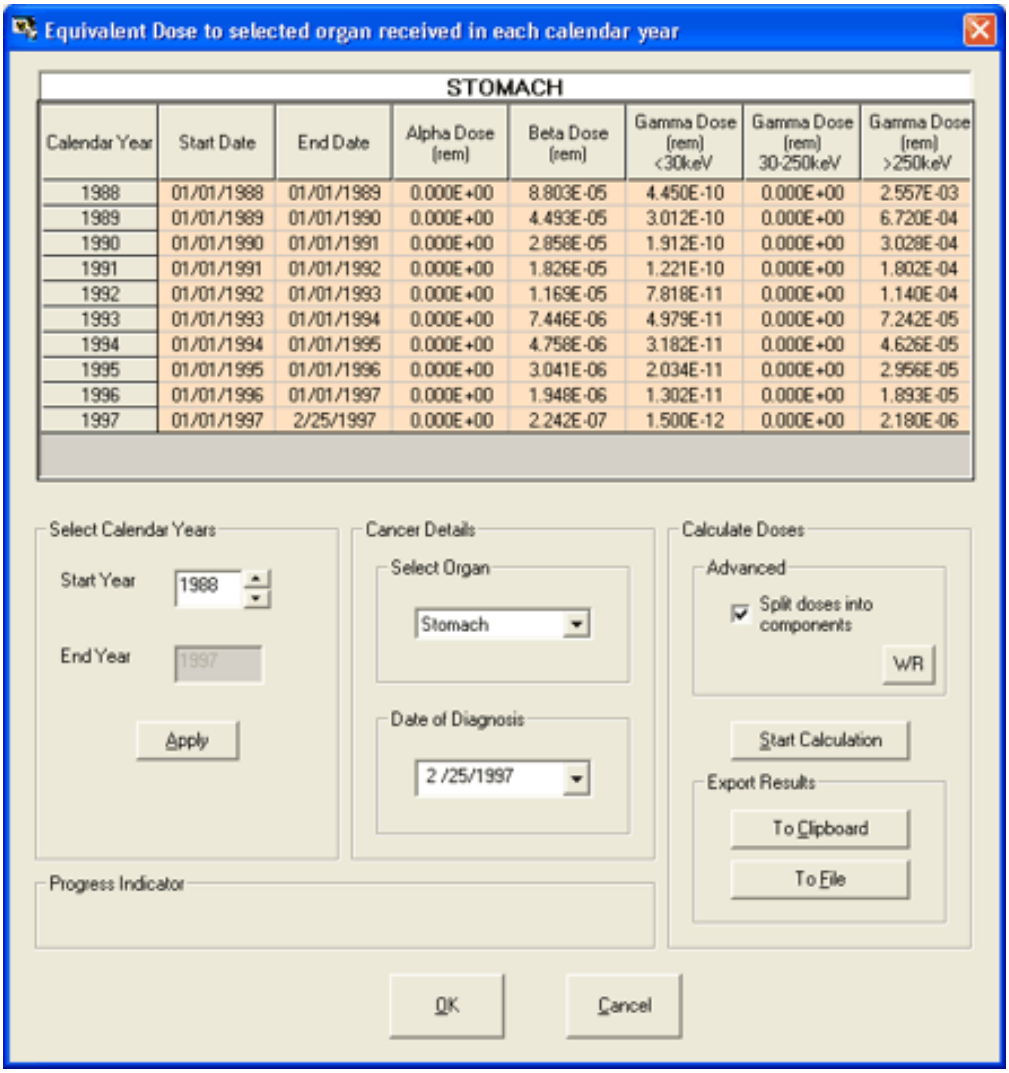


Figure 8.5. '**Split**' components of annual equivalent doses displayed for the stomach wall.

Important Note: The values of radiation weighting factor used by IMBA Expert™ OCAS/ORAU-Edition to calculate the annual equivalent dose are shown by clicking the '**WR**' button (Figure 8.5). These 'standard' values (Figure 8.6) are those currently required by **NIOSH-OCAS -** and MUST NOT be changed. The NIOSH-IREP program automatically applies the required pre-defined 'weighting' distributions (as multipliers) to evaluate the corresponding uncertainty distributions of equivalent dose.

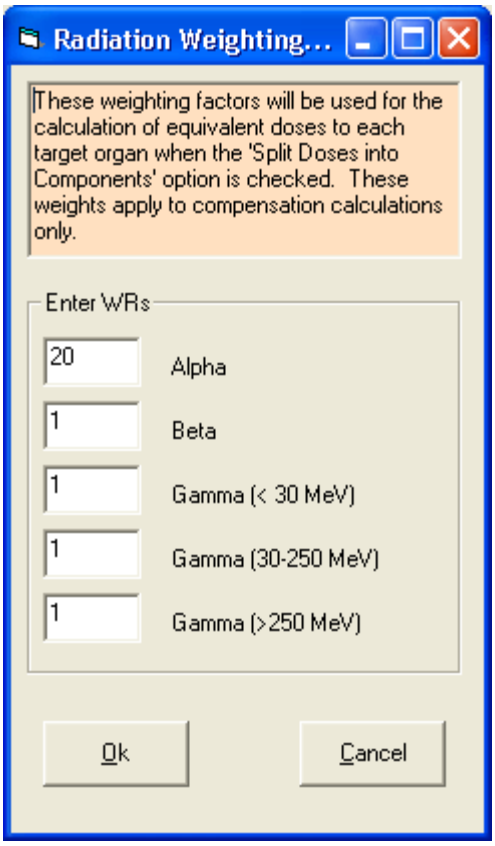


Figure 8.6. Standard values of radiation weighting factor used to calculate '**split**' annual equivalent doses.

Important Note: IMBA Expert™ OCAS/ORAU-Edition (Version 4.0) calculates annual equivalent doses ONLY for the **Indicator Nuclide**. Annual doses from any **Associated Radionuclide(s)**, must be calculated separately for the corresponding intake amount(s) - and intake regimes - and *summed* (year-by-year) before entry into the NIOSH-IREP program.

8.1.2. Summing Annual Doses Calculated for Associated Radionuclides

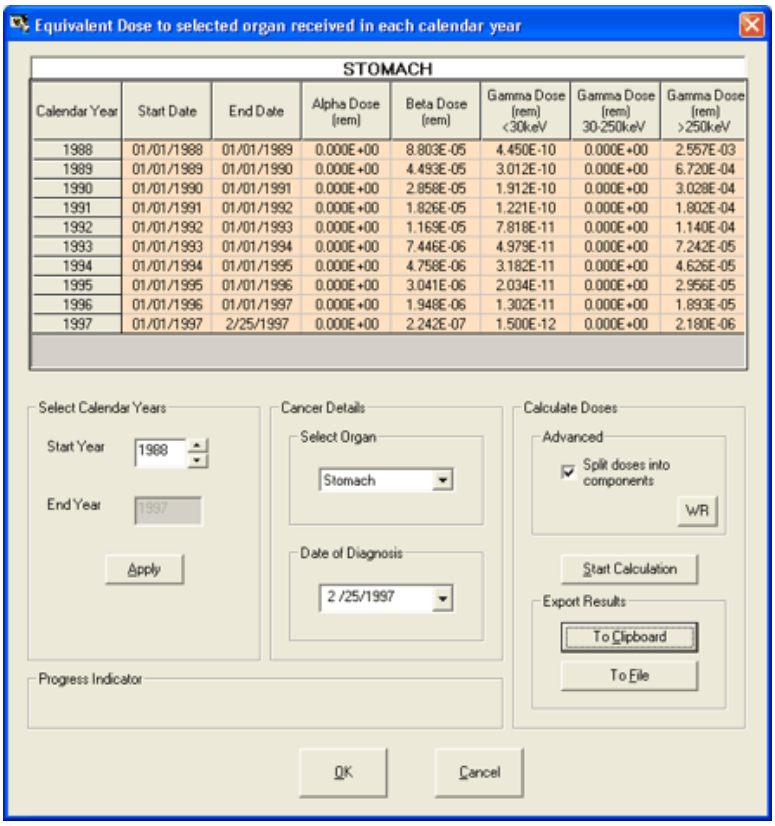


Figure 8.7. The '**Export Results - To Clipboard**' button.

Clicking the '**Export Results - To Clipboard**' button (Figure 8.7) *copies* the displayed table of calculated annual equivalent doses to the Windows® clipboard. These data can then be pasted into any Windows® spreadsheet (or database) application - as in Figure 8.8.

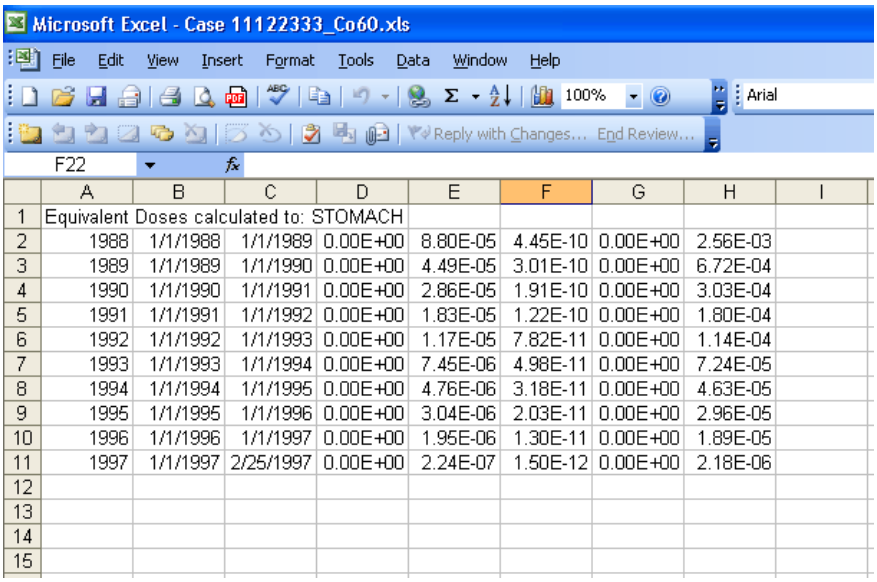


Figure 8.8. Calculated 'split' annual equivalent doses imported into a spreadsheet.

The Windows® spreadsheet (or database) application can be used to *add* the annual doses calculated (separately) for ALL **Associated Radionuclides**. The resulting total annual equivalent doses can then be copied and pasted directly into the NIOSH-IREP input file - by-passing part of the function of '**FeedIREP**'.

As an alternative to copying the calculated results directly to a Windows® spreadsheet (or database) application (using the Windows® clipboard), you can export the calculated data table to an **ASCII (*.txt) file**.

8.1.3. Exporting to an ASCII Data File

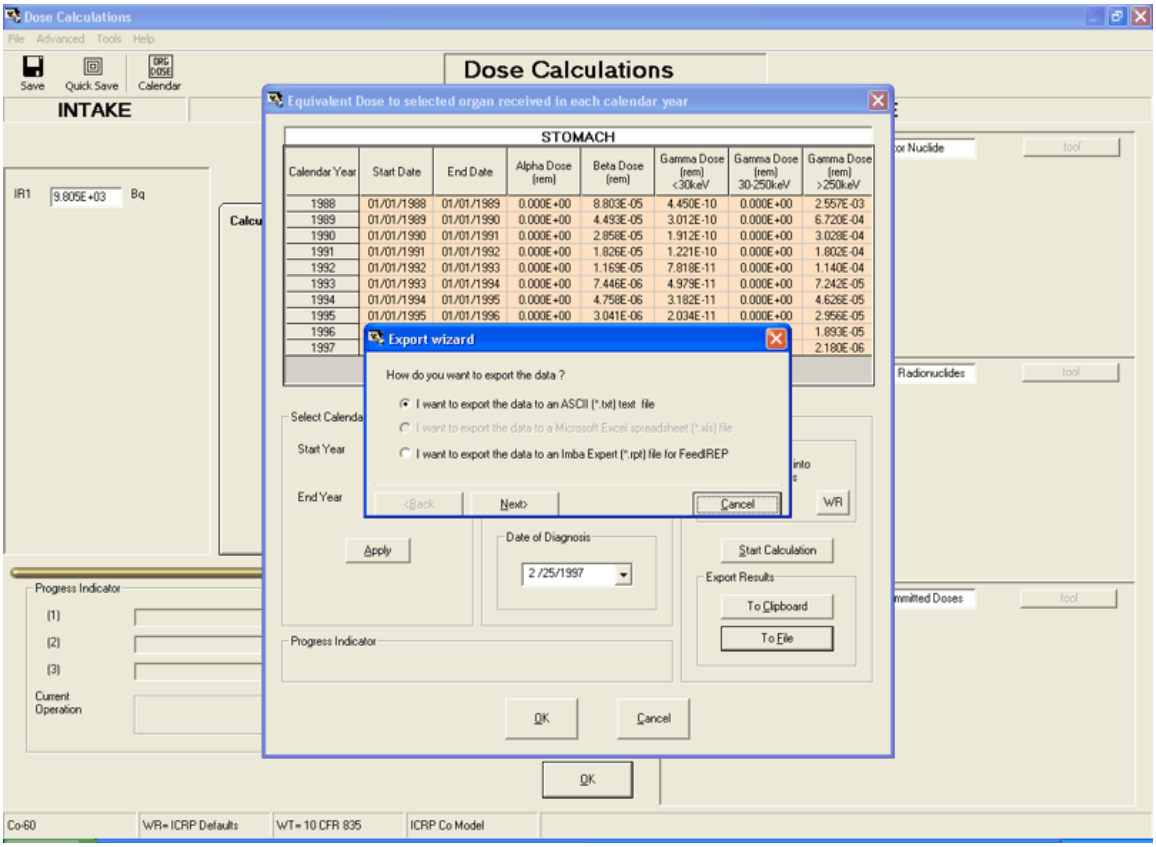


Figure 8.9. Opening the '**Export Wizard**'.

IMBA Expert™ OCAS/ORAU-Edition provides an '**Export Wizard**' (Figure 8.10) that is opened in the '**Equivalent Dose to selected organ received in each calendar year**' window. This enables the calculated annual doses to be exported to:

- an ASCII (***.txt**) file, or;
- an IMBA Expert (***.rpt**) file for '**FeedIREP**'.

Exporting to an ASCII (*.txt) File

With the '**I want to export the data to an ASCII (*.txt) text file**' option checked (the default), *clicking* the '**Next**' button opens '**Please specify the name and location of the ASCII file you want to create**' *browse* option in the ' **Export Wizard**' (Figure 8.10).

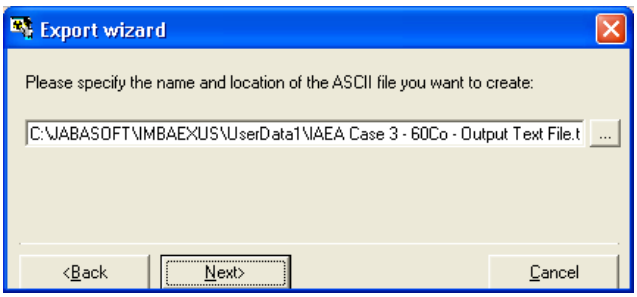

Export wizard
Please specify the name and location of the ASCII file you want to create:
C:\JABASOFT\IMBAEXUS\UserData1\IAEA Case 3 - 60Co - Output Text File.t
...
<Back
Next>
Cancel

Figure 8.10. Specifying the name and location of the ASCII (***.txt**) output text file.

You simply *browse* to the folder where you want to store the output (***.txt**), and *name* the file. *Clicking* the '**Next**' button enables you to *select* the type of *text delimiter* that you want to use (Figure 8.11).

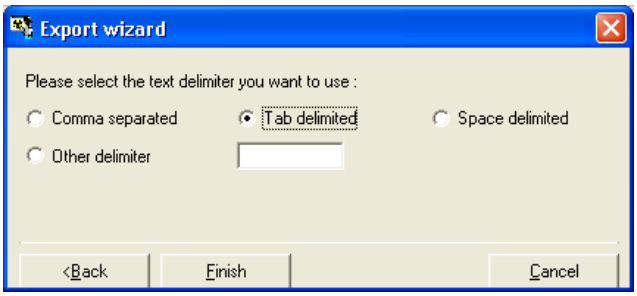


Figure 8.11. Selection of a '**Tab delimited**' output (***.txt**) file.

In this example we have selected a '**Tab delimited**' output file. *Clicking* the '**Finish**' button completes the data export process. Successful export of the data will be confirmed (Figure 8.12), and *clicking* the '**View File ...**' button will *display* the resulting (***.txt**) file (Figure 8.13) in NotePad®.

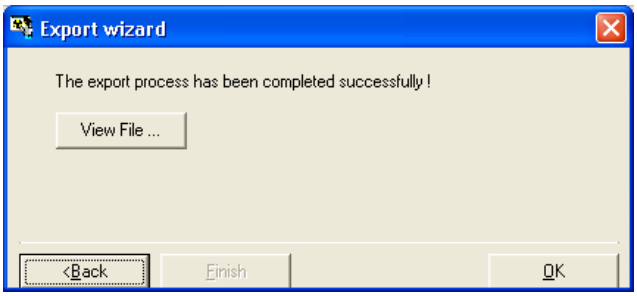


Figure 8.12. Confirmation of successful data export to a (***.txt**) file.

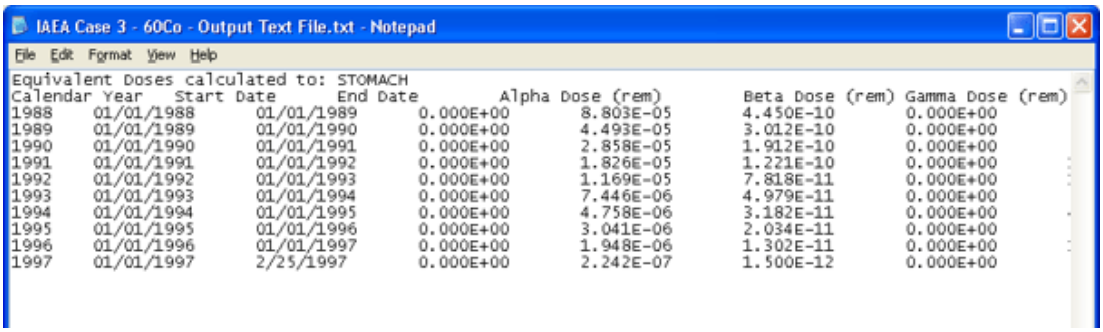


Figure 8.13. Resulting (***.txt**) file displayed in NotePad®.

Note: The exported (***.txt**) file contains only the results of the last-performed calculation of annual equivalent doses. You will have to *add* other information, such as the identity of the indicator nuclide, or other case details. IMBA Expert™ OCAS/ORAU-Edition can *add* such case information automatically - in a file format that can be *fed directly* to '**FeedIREP**' – see the following sections: "**Input '*.ini' File**" and "**Incorporating the '*.ini' File Data**".

8.2. The Input '*.ini' File – and How to Use It

```
; IMBA/IREP COnfiguration File

: Introductory Header

; This configuration file is used by the IMBA and FeedIREP programs
to provide
; case header information which will be used to populate selected
fields in
; the applications, and set defaults for various controls within
the programs,
; such as check buttons.

; NOTICE: The information contained in this file is protected by
; Privacy Act 5 USC Section 552a; disclosure to any third party
without
; the written consent of the individual to whom the information
pertains
; is strictly prohibited.

[Claimant Information]
NIOSHID=999999
FirstName=John
MiddleName=C.
LastName=Smith
SSN=111-22-3333
DOB=02/25/1950
Gender=M
DOLOffice=DE
SmokingHistory=Never Smoked
Ethnicity=White-Non-Hispanic
Cancer1=Stomach (151)
Cancer1DiagnosisDate=02/25/1997
Cancer1Rank=1

[General Details]
AdministrativeDetails=T
SoftwareVersion=T
ParameterFilename=T

[Input Information]
IndicatorRadionuclide=T
AssociatedRadionuclide=F
IntakeRegimes=T
ModelParameters=T
MeasurementData=T
RadiationWeightingFactors=F
TissueWeightingFactors=F

[Results of Calculations]
Intakes=T
BioassayResults=T

[Indicator Radionuclide]
EquivalentDoses=F
EffectiveDoses=F

[Associated Radionuclides]
EquivalentDoses=F
EffectiveDoses=F

[Calendar Year Doses]
EquivalentDoses=T
```

Figure 8.14. Standard **'Case Configuration File'** (***.INI**) used to import **Case Information** into IMBA Expert™ OCAS/ORAU-Edition.

The detailed specification of the data fields in the **'Case Configuration File**' (*.ini) is proprietary to Oak Ridge Associated Universities, Inc. and MJW Corporation Inc. This specification was incorporated into IMBA Expert™ OCAS/ORAU-Edition, to enable the software to import all of the claimant-specific information in the precise form needed to pass through to the **NIOSH-IREP** program.

Figure 8.14 shows the general layout of the '***.ini**' file. We describe here how to **import** this file into IMBA Expert™ OCAS/ORAU-Edition.

	Important Notice: The information contained in the '*.INI' file is protected by Privacy Act 5 USC Section 552a; disclosure to any third party without the written consent of the individual to whom the information pertains is strictly prohibited
	Note: The example **"*.ini**" files used here are purely for the purpose of illustrating the operation of IMBA Expert™ OCAS/ORAU-Edition. They utilize previously published bioassay data. They contain NO personal information - and are NOT associated in any way with any identified individual claimant. The identifying file names are arbitrary.

8.2.1. Incorporating the '*.ini' File Data

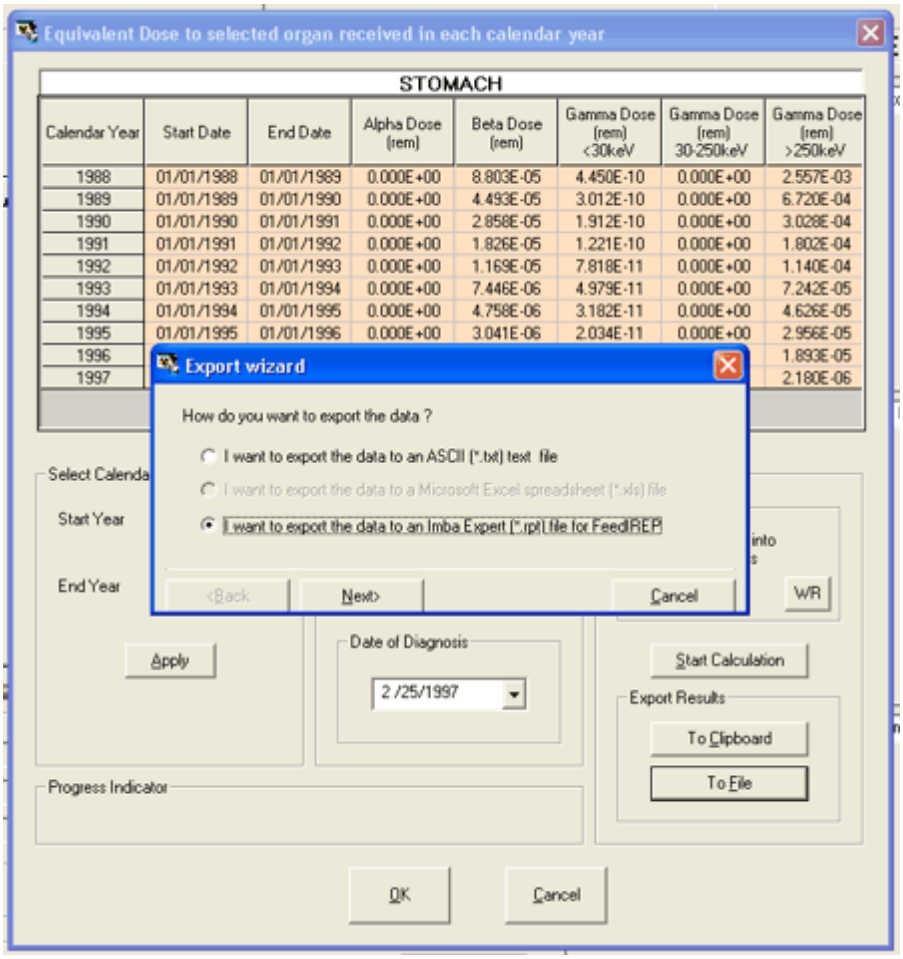

Equivalent Dose to selected organ received in each calendar year
STOMACH
Calendar Year
Start Date
End Date
Alpha Dose (rem)
Beta Dose (rem)
Gamma Dose (rem) <30keV
Gamma Dose (rem) 30-250keV
Gamma Dose (rem) >250keV
1988 01/01/1988 01/01/1989 0.000E+00 8.803E-05 4.450E-10 0.000E+00 2.557E-03
1989 01/01/1989 01/01/1990 0.000E+00 4.493E-05 3.012E-10 0.000E+00 6.720E-04
1990 01/01/1990 01/01/1991 0.000E+00 2.858E-05 1.912E-10 0.000E+00 3.028E-04
1991 01/01/1991 01/01/1992 0.000E+00 1.826E-05 1.221E-10 0.000E+00 1.802E-04
1992 01/01/1992 01/01/1993 0.000E+00 1.169E-05 7.818E-11 0.000E+00 1.140E-04
1993 01/01/1993 01/01/1994 0.000E+00 7.446E-06 4.979E-11 0.000E+00 7.242E-05
1994 01/01/1994 01/01/1995 0.000E+00 4.758E-06 3.182E-11 0.000E+00 4.626E-05
1995 01/01/1995 01/01/1996 0.000E+00 3.041E-06 2.034E-11 0.000E+00 2.956E-05
1996 1.893E-05
1997 2.180E-06
Export wizard
How do you want to export the data ?
I want to export the data to an ASCII (*.txt) text file
I want to export the data to a Microsoft Excel spreadsheet (*.xls) file
I want to export the data to an Imba Expert (*.rpt) file for FeedIREP
<Back
Next>
Cancel
Select Calenda
Start Year
End Year
Apply
Date of Diagnosis
2 /25/1997
Start Calculation
Export Results
To Clipboard
To File
Progress Indicator
OK
Cancel

Figure 8.15. Using the '**Export Wizard**' to export data directly to a (***.rpt**) file - formatted for '**FeedIREP**'.

The '**Export Wizard**' enables you to export calculated annual equivalent doses to a (***.rpt**) file that is formatted for *direct* input into '**FeedIREP**' (Figure 8.15). This method of exporting the calculated results has two advantages:

1. Personal information about the claimant (from the approved *standard* format **Initiation file** - '***.ini**') is *automatically* combined with the calculated doses in the output (***.rpt**) file.

2. ALL details of the intake and dose assessment that you have performed can also be *automatically* included (and thus *recorded*) in the (***.rpt**) file.

Checking the '**I want to export the data to an IMBA Expert (*.rpt) file for FeedIREP**' and *clicking* the ' **Next** ' button (Figure 8.15) opens the Export Wizard's '**Browse**' dialog box (Figure 8.16). Use this to find, and load, the required **Initiation file** (***.ini**). In this example, we are using the file "**C:\JABASOFT\IMBAEXUS\UserData1\11122333_Co60.ini**".

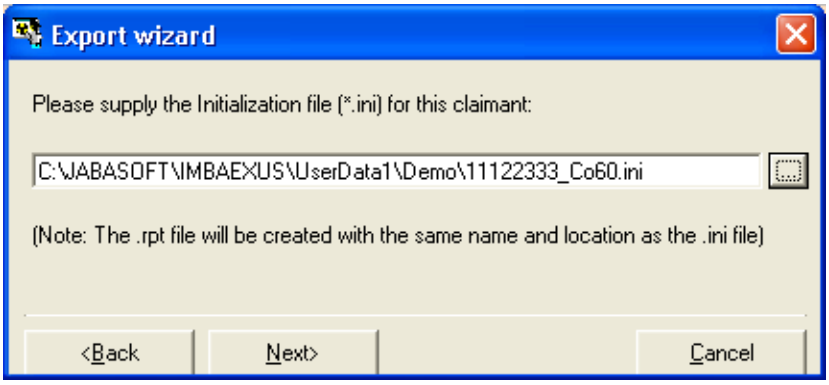

Export wizard
Please supply the Initialization file (*.ini) for this claimant:
C:\JABASOFT\IMBAEXUS\UserData1\Demo\11122333_Co60.ini
(Note: The .rpt file will be created with the same name and location as the .ini file)
<Back
Next>
Cancel

Figure 9.16. Browsing to locate the **Initiation file** (***.ini**).

Note: In ORAU's Energy Employees Occupational Illness Compensation Program Dose Reconstruction Project, the name of the **Initiation file** is composed of two parts (1) the **NIOSH Claim number** - full 6 digits with leading zeros, and (2) the file extension '**.ini**'. For example, '**000251.ini**' is a valid file name.

Once you have located the '***.ini**' file, *clicking* '**Next**' in the 'Export Wizard' will ask you "**How do you want to configure the *.rpt file?**" (Figure 8.17). The *default* option is "**Automatically**" - and this is RECOMMENDED for compatibility with '**FeedIREP**'.

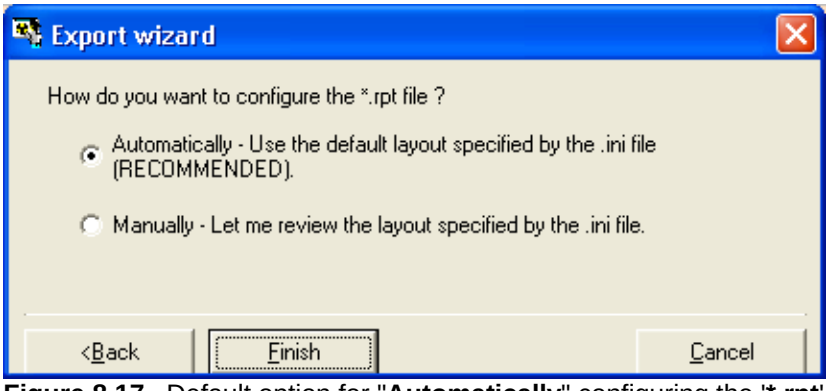

Export wizard
How do you want to configure the *.rpt file ?
Automatically - Use the default layout specified by the .ini file (RECOMMENDED).
Manually - Let me review the layout specified by the .ini file.
<Back
Finish
Cancel

Figure 8.17. Default option for "**Automatically**" configuring the '***.rpt**' file.

Clicking '**Finish**' will complete the export process. The resulting **'*.rpt'** file can be *viewed* by clicking the '**View File ...**' button (Figure 8.18.).

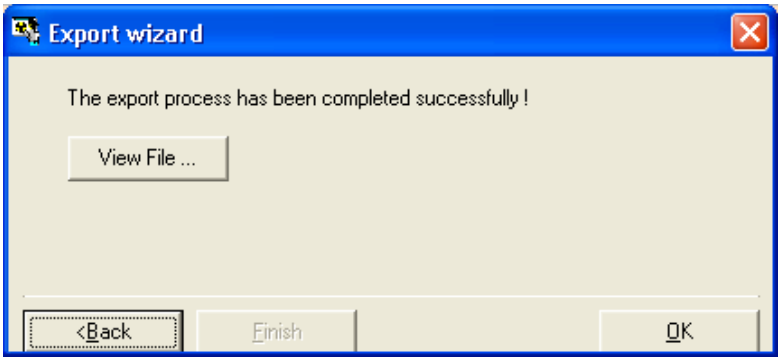


Figure 8.18. Confirmation of successful export of a '***.rpt'** file.

	Note #1: The *output* '***.rpt'** file is automatically saved in the same folder as the *input* '***.ini'** file.
	Note #2: The resulting '***.rpt**' file is shown in "Output to 'FeedIREP'".

8.3. Standard-format Output to 'FeedIREP'

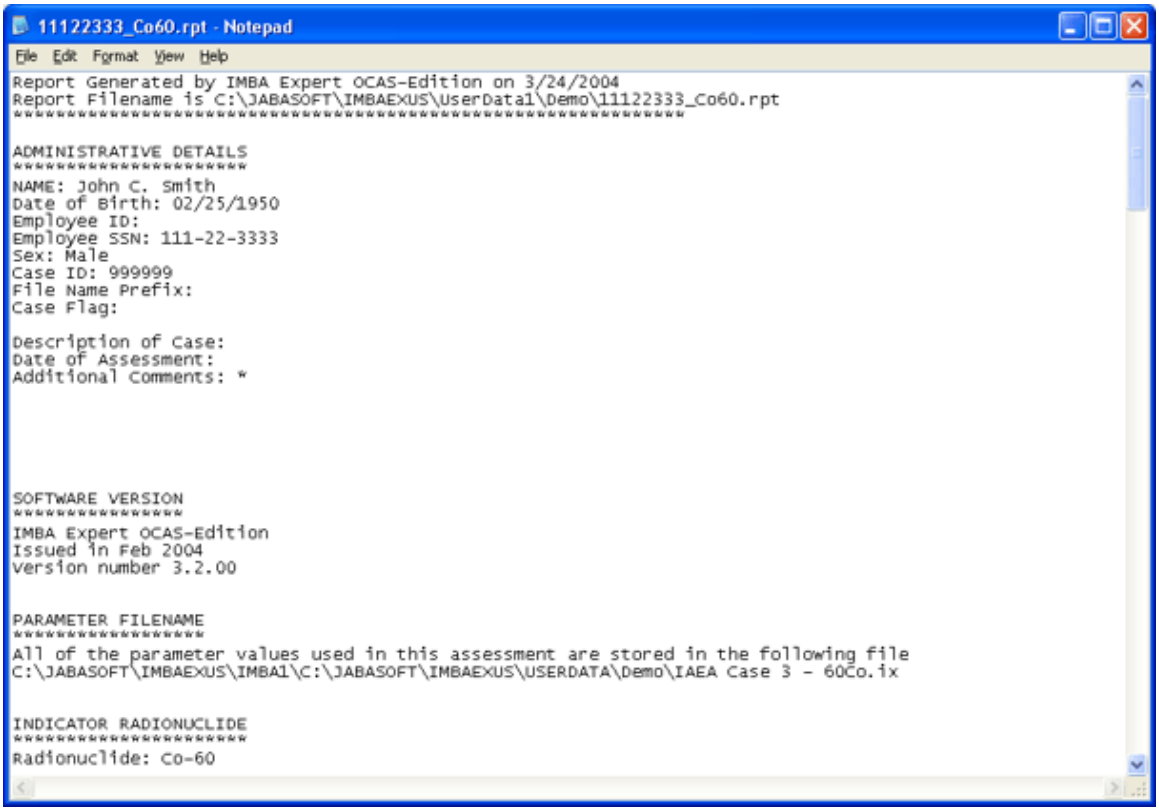


Figure 8.19. '**11122333_Co60.rpt**' file produced for the example case - as viewed in NotePad®.

The complete '**11122333_Co60.rpt**' file listing is:

```
Report Generated by IMBA Expert OCAS-Edition on 3/24/2004
Report Filename is C:\JABASOFT\IMBAEXUS\UserData1\Demo\11122333_Co60.rpt
************************************************************

ADMINISTRATIVE DETAILS
**********************
NAME: John C. Smith
Date of Birth: 02/25/1950
Employee ID:
Employee SSN: 111-22-3333
Sex: Male
Case ID: 999999
File Name Prefix:
Case Flag:

Description of Case:
Date of Assessment:
Additional Comments: *



SOFTWARE VERSION
****************
IMBA Expert OCAS-Edition
Issued in Feb 2004
Version number 3.2.00


PARAMETER FILENAME
******************
All of the parameter values used in this assessment are stored in the following
file
C:\JABASOFT\IMBAEXUS\IMBA1\C:\JABASOFT\IMBAEXUS\USERDATA\Demo\IAEA Case 3 -
60Co.ix


INDICATOR RADIONUCLIDE
**********************
Radionuclide: Co-60
Halflife: 1924 (d)


INTAKE REGIMES
**************
There is only one intake regime
Intake  1 :acute inhalation on day  0


MODEL PARAMETERS
****************
The following model parameters are different for each intake regimes

INTAKE REGIME  1

Aerosol/deposition parameters were: User Defined
AMAD         =1 µm
GSD          = 2.47
Density      =3g/cc
Shape Factor = 1.5
Worker Type  =light
```

```
Absorption to blood was:Type M
Fr= 9.99549977498875E-02
Sr=100
Ss= 0.005
Fb=0
Sb=0

Particle transport parameters were ICRP Defaults
AI1   to  bb1   = 0.02
AI2   to  bb1   = 0.001
AI3   to  bb1   = 0.0001
AI3   to  LNTH  = 0.00002
bb1   to  BB1   = 2
bb2   to  BB1   = 0.03
bbseq to  LNTH  = 0.01
BB1   to  ET2   = 10
BB2   to  ET2   = 0.03
BBseq to  LNTH  = 0.01
ET2   tO  GI    = 100
ETseq to  LNET  = 0.001
ET1   out         1

Initial deposition partitioning
ETseq/ET2 = 0.0005
BBseq/BB  = 0.007
bbseq/bb  = 0.007
AI2/AI    = 0.6
AI3/AI    = 0.1

GI-tract parameters were ICRP Defaults
Stomach (ST)                =  24
Small intestine (SI)        =  6
Upper Large Intestine (ULI) =  1.8
Lower Large Intestine (LLI) =  1
Absorption to Blood (f1)    =  0.1

Biokinetic model parameters were ICRP Co Model
Organ/tissue retention functions were as follows:

LIVER
a(i),         lam(i)
-5.281760000000000E-02, 1.386290000000000E+00
 3.272730000000000E-02, 1.155250000000000E-01
 1.008400000000000E-02, 1.155250000000000E-02
 1.000630000000000E-02, 8.664340000000000E-04
Fraction to urine 8.571430000000000E-01

SOFT TISS
a(i),         lam(i)
-4.753576000000000E-01, 1.386290000000000E+00
 2.945450000000000E-01, 1.155250000000000E-01
 9.075630000000000E-02, 1.155250000000000E-02
 9.005630000000000E-02, 8.664340000000000E-04
Fraction to urine 8.571430000000000E-01

BLOOD
a(i),         lam(i)
 1.000000000000000E+00, 1.386290000000000E+00
Fraction to urine 8.571430000000000E-01

Bioassay function for Whole body was Std Co Model
a(i),         lam(i)
```

```
 5.301073120979730E-01, 1.000000000000000E+00
 3.397310000000000E-01, 1.155250000000000E-01
-3.019360000000000E-01, 1.386290000000000E+00
 2.864620000000000E-01, 1.800000000000000E+00
 1.011860000000000E-01, 1.155250000000000E-02
 1.000880000000000E-01, 8.664340000000000E-04
-5.563920000000000E-02, 1.200000000000000E+01
Blood retention:  1.0000E-07

Bioassay function for Urine was Std Co Model
a(i),         lam(i)
-6.676703004002170E-01, 1.200000000000000E+01
 6.338750000000000E-01, 1.386290000000000E+00
 3.272190000000000E-02, 1.155250000000000E-01
 9.994940000000000E-04, 1.155250000000000E-02
 7.431760000000000E-05, 8.664340000000000E-04
Blood retention:  1.0000E-07

Bioassay function for Feces was Std Co Model
a(i),         lam(i)
-1.052446700679250E+00, 1.386290000000000E+00
 5.301070000000000E-01, 1.000000000000000E+00
 5.156320000000000E-01, 1.800000000000000E+00
 6.525410000000000E-03, 1.155250000000000E-01
 1.694540000000000E-04, 1.155250000000000E-02
 1.240210000000000E-05, 8.664340000000000E-04
Blood retention:  1.0000E-07


MEASUREMENT DATA
****************
Whole body data
1.  ,    ,  2720  ,  Real  ,  272  ,  NORM  ,  3334.2
6.  ,    ,  1150  ,  Real  ,  115  ,  NORM  ,  1195.9
16.  ,    ,  1010  ,  Real  ,  101  ,  NORM  ,  1007.7
33.  ,    ,  790  ,  Real  ,  79  ,  NORM  ,  828.3
82.  ,    ,  482  ,  Real  ,  48.2  ,  NORM  ,  555.59
169.  ,    ,  358  ,  Real  ,  35.8  ,  NORM  ,  338.12
1009.  ,    ,  78  ,  Real  ,  7.8  ,  NORM  ,  37.122
1456.  ,    ,  35  ,  Real  ,  3.5  ,  NORM  ,  20.779

During the fitting procedure, the following data were used:


BIOASSAY RESULTS
****************
Whole body results
Time,         N/A,          Value
d,            ,             Bq
1  ,    ,  3334.2
1.4671759259254  ,    ,  2683.8
2.1526041666657  ,    ,  2032.1
3.15825231481358  ,    ,  1540
4.63370370370467  ,    ,  1278.4
6.79846064814774  ,    ,  1169.2
9.97454861110964  ,    ,  1101.1
14.6344097222209  ,    ,  1026.9
21.4712499999987  ,    ,  939.97
31.5021064814828  ,    ,  841.05
46.2191319444428  ,    ,  731.49
67.8115972222222  ,    ,  614.57
99.4915393518531  ,    ,  495.85
145.971585648149  ,    ,  380.5
```

```
214.165983796298  ,    ,  272.57
314.219155092593  ,    ,  178.78
461.014768518518  ,    ,  108.29
676.389756944445  ,    ,  63.956
992.382731481484  ,    ,  38
1456  ,    ,  20.779


INTAKES
*******
Intake 1 was 9804.8 Bq


EQUIVALENT DOSE to Stomach (Sv) from the Indicator Radionuclide (Co-60) in each
calendar year
********************************************************************************
************
year,         alpha,        beta,         gamma1,       gamma2,       gamma3,
1988,         0.000E+00,    8.803E-07,    4.450E-12,    0.000E+00,    2.557E-05,
1989,         0.000E+00,    4.493E-07,    3.012E-12,    0.000E+00,    6.720E-06,
1990,         0.000E+00,    2.858E-07,    1.912E-12,    0.000E+00,    3.028E-06,
1991,         0.000E+00,    1.826E-07,    1.221E-12,    0.000E+00,    1.802E-06,
1992,         0.000E+00,    1.169E-07,    7.818E-13,    0.000E+00,    1.140E-06,
1993,         0.000E+00,    7.446E-08,    4.979E-13,    0.000E+00,    7.242E-07,
1994,         0.000E+00,    4.758E-08,    3.182E-13,    0.000E+00,    4.626E-07,
1995,         0.000E+00,    3.041E-08,    2.034E-13,    0.000E+00,    2.956E-07,
1996,         0.000E+00,    1.948E-08,    1.302E-13,    0.000E+00,    1.893E-07,
1997,         0.000E+00,    2.242E-09,    1.500E-14,    0.000E+00,    2.180E-08,

Note(A):  The calendar dose in  1997 is that received up to 2/25/1997
          because this is when the cancer was diagnosed.
Note(B):  The additional energy from the nucleus caused by alpha recoil has
          been included where necessary
Note(C):  These calculations have been optimised for accuracy
Note(D):  gamma1 = 30 keV, gamma2 = 30-250 keV, gamma3 = >250keV
```

Note: Consult the approved operating procedure documentation for ORAU's Energy Employees Occupational Illness Compensation Program Dose Reconstruction Project for instructions on how to use '**FeedIREP**' to read the '***.rpt**' file formatted by IMBA Expert™ OCAS/ORAU-Edition - and also the '**User's Guide**' to *run* **NIOSH-IREP**.

9. References

Doerfel H, Andrasi A, Bailey MR, Berkovski V, Castellani C-M, Hurtgen C, Jourdain J-R, Le Guen B. Guidance on internal dose assessments from monitoring data (Project IDEAS). Presented at the Workshop on Internal Dosimetry of Radionuclides, Occupational, Public and Medical Exposure, Oxford, 9-12 September 2002. Radiat. Prot. Dosim. 105(1-4):645-647; 2003.

EEOICPA (2000): The Energy Employees' Occupational Illness Compensation Program Act (EEOICPA), Public Law 106-398, 113 Stat. 1654A-1231 (October 30, 2000)

International Commission on Radiological Protection. Human respiratory tract model for radiological protection. Oxford: Elsevier Science Ltd; *ICRP Publication 66*; Ann ICRP 24(1-3); 1994a.

International Commission on Radiological Protection. Basic anatomical and physiological data for use in radiological protection: Reference values. Elsevier Science Ltd; *ICRP Publication 89*; Ann ICRP 32(3-4); 2002b.

James AC, Filipy RE, Russell JJ, McInroy JF. USTUR Case 0259 whole body donation: A comprehensive test of the current ICRP models for the behavior of inhaled $^{238}PuO_2$ ceramic particles. Health Phys. 84(1):3-33; 2003.

Miller G, Inkret W C, Martz H F. Internal dosimetry intake estimation using Bayesian methods. Radiat Prot Dosim. 82:5–17; 1999.

NIOSH-IREP (2003): User's Guide for the Interactive RadioEpidemiology Program (NIOSH-IREP). Version 5.2; January 15, 2003; Oak Ridge, TN: SENES Oak Ridge, Inc.